

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 14:38:46 : Search time 70 Seconds
(without alignments)
171.343 Million cell updates/sec

Title: US-10-664-605-5

Perfect score: 68

Sequence: 1 CFGXXXXRIGXXXXGC 17

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trernbl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	83.8	106	2	06VYM3 BRARE
2	57	83.8	142	1	ANF_ACTR
3	57	83.8	146	2	Q7T217 ONCMY
4	57	83.8	148	2	Q78AW6 SALSA
5	57	83.8	152	2	Q9YGI1 SALSA
6	56	82.4	30	1	ANF_RANRI
7	56	82.4	83	2	Q4TD23 TETNG
8	56	82.4	128	1	ANF_CAVPO
9	56	82.4	133	1	ANF_FUGRU
10	56	82.4	138	1	ANF_OREMO
11	56	82.4	139	2	Q4T953 TETNG
12	56	82.4	139	1	ANF_FUGRU
13	56	82.4	140	1	ANF_OREMO
14	56	82.4	145	1	ANF_RANCA
15	56	82.4	145	2	Q5XFR8_RANRI
16	56	82.4	146	1	Q7TIQ2_ORYLA
17	56	82.4	150	1	ANF_ACTR
18	56	82.4	159	2	Q90X61_BUFMA
19	55	80.9	22	1	ANFC_CHICK
20	55	80.9	25	2	Q4SND6 TETNG
21	55	80.9	27	1	ANF_ANGJA
22	55	80.9	33	2	Q9QZ96_CAVPO
23	55	80.9	37	1	PNFP_PSEPC
24	55	80.9	38	2	Q7LZ09_VIPLE
25	55	80.9	101	2	Q4S797 TETNG
26	55	80.9	103	1	ANFB_BOVIN
27	55	80.9	112	2	Q9GLK5_FELCA
28	55	80.9	115	1	ANFC_SCYCA
29	55	80.9	118	1	ANFD_RANCA
30	55	80.9	120	1	ANFC4_FUGRU
31	55	80.9	121	1	ANFB_MOUSE

32	55	80.9	121	1	ANFB_RAT	P13205 rattus norv
33	55	80.9	121	1	ANFC4_ORYLA	Q80017 oryzias lat
34	55	80.9	121	2	Q794A8_MOUSE	Q794A8 mus muscul
35	55	80.9	121	2	Q91V40_MUSST	Q91V40 mus spicile
36	55	80.9	121	2	Q54AB9_MOUSE	Q54AB9 mus muscul
37	55	80.9	121	2	Q55086_MOUSE	Q55086 mus muscul
38	55	80.9	126	1	ANFC1_FUGRU	Q805d6 fugu rubrip
39	55	80.9	126	1	ANFC2_ORYLA	Q805e7 orochromis
40	55	80.9	126	1	ANFC_BOVIN	Q805e7 fugu rubrip
41	55	80.9	126	1	ANFC_HUMAN	Q805e7 fugu rubrip
42	55	80.9	126	1	ANFC_MOUSE	Q805e7 fugu rubrip
43	55	80.9	126	1	ANFC_PIG	Q805e7 fugu rubrip
44	55	80.9	126	1	ANFC_RAT	Q805e7 fugu rubrip
45	55	80.9	126	1	ANFC_SHEEP	Q805e7 fugu rubrip
46	55	80.9	126	2	Q4ZG41_HUMAN	Q4ZG41 homo sapien
47	55	80.9	126	2	Q544K5_MOUSE	Q544K5 mus muscul
48	55	80.9	129	1	ANFB_SHEEP	Q46541 ovis aries
49	55	80.9	129	1	ANFC_RANCA	P20968 rana cateab
50	55	80.9	130	1	ANFC2_FUGRU	Q805d5 fugu rubrip
51	55	80.9	131	1	ANFB_PIG	P07634 sus scrofa
52	55	80.9	131	1	ANFC1_ONCMY	Q8axr3 oncorhynch
53	55	80.9	131	1	ANFC1_ORYLA	Q8ayr6 oryzias lat
54	55	80.9	131	1	ANFC2_ONCMY	Q8axr2 oncorhynch
55	55	80.9	131	1	ANFC_ANGJA	P18145 anguilla ja
56	55	80.9	131	2	Q805E7_OREMO	Q805e7 orochromis
57	55	80.9	132	1	ANFB_FELCA	Q9GLK4 felis silve
58	55	80.9	132	2	Q6L7Z3_CAMDR	Q6L7Z3 camelus dro
59	55	80.9	135	1	ANFC_SQUAC	P41319 squalus aca
60	55	80.9	136	1	ANFC_TRIAC	P55208 triakis scy
61	55	80.9	140	1	ANFB_CANPA	P16859 canis famil
62	55	80.9	140	1	ANF_CHICK	P18908 gallus gall
63	55	80.9	140	2	Q9PSV1_ANGJA	Q9PSV1 anguilla ja
64	55	80.9	144	2	Q805B6_FUNHE	Q805b6 fundulus he
65	55	80.9	147	2	Q8VHG9_NOTAL	Q8VHG9 notomys ale
66	55	80.9	147	2	Q9DGH8_XENLA	Q9DGH8 xenopus lae
67	55	80.9	149	1	ANF_CANPA	P07499 canis famil
68	55	80.9	150	1	ANFC_ACTR	Q76Kw6 acipenser t
69	55	80.9	150	1	ANFB_ANGJA	P22642 anguilla ja
70	55	80.9	150	1	ANF_PIG	P24259 sus scrofa
71	55	80.9	151	2	Q5JZEL_HUMAN	Q5JZEL homo sapien
72	55	80.9	152	1	ANF_BOVIN	P07501 bos taurus
73	55	80.9	152	1	ANF_MOUSE	P05125 mus muscul
74	55	80.9	152	1	ANF_RAT	P01161 rattus norv
75	55	80.9	152	1	ANF_SHEEP	Q64540 ovis aries
76	55	80.9	152	2	Q6L7Z4_CAMDR	Q6L7Z4 camelus dro
77	55	80.9	152	2	Q9TOW1_BALPH	Q9TOW1 balaeopter
78	55	80.9	152	2	Q5FW59_MOUSE	Q5FW59 mus muscul
79	55	80.9	152	2	Q8VHH2_NOTAL	Q8VHH2 notomys ale
80	55	80.9	153	1	ANF_FELCA	Q9GLK4 felis silve
81	55	80.9	153	1	ANF_HORSE	P21104 equus cabal
82	55	80.9	153	1	ANF_HUMAN	P01160 homo sapien
83	55	80.9	153	1	ANF_RABIT	P07500 oryctolagus
84	55	80.9	155	2	Q29130_TUPGB	Q29130 tupai glis
85	55	80.9	181	2	Q90Y11_CRODU	Q90Y11 cretalis du
86	55	80.9	181	2	Q90Y12_CRODU	Q90Y12 cretalis du
87	55	80.9	221	2	Q7T1M4_BOTUR	Q7T1M4 bothrops ja
88	55	80.9	226	2	Q6LEW5_BOTUR	Q6LEW5 bothrops ja
89	55	80.9	263	2	Q9PT52_AKHA	Q9PT52 agkistrodon
90	55	80.9	265	2	Q8QG91_BOTIN	Q8QG91 bothrops in
91	55	80.9	265	2	Q9PM56_BOTJA	Q9PM56 bothrops ja
92	55	80.9	277	2	Q4TBD2_TETNG	Q4TBD2 terradon n
93	54	79.4	39	1	VNOC_OXYMI	P83230 oxyuranus m
94	54	79.4	39	1	VNOC_OXYSA	P83231 oxyuranus s
95	54	79.4	104	2	Q6DF98_XENLA	Q6DF98 xenopus lae
96	53	77.9	162	2	Q7YZUS_EPTBU	Q7YZUS eptatretus
97	51	75.0	112	1	ANFC3_ORYLA	Q80108 oryzias lat
98	51	75.0	145	1	ANFB_ACTR	P83962 acipenser t
99	50	73.5	35	2	Q9PRU2_ONCMY	Q9PRU2 oncorhynch
100	50	73.5	134	1	ANFB_HUMAN	P18860 homo sapien
101	50	73.5	134	2	Q6FGY0_HUMAN	Q6FGY0 homo sapien
102	50	73.5	149	2	Q7T216_ONCMY	Q7T216 oncorhynch
103	49	72.1	35	1	VNOA_OXYMI	P83224 oxyuranus m
104	49	72.1	35	1	VNOA_OXYSA	P83226 oxyuranus s

105	49	72.1	35	1	VNOA_OXYSC	P83225 oxyturanus s	178	33.5	49.3	178	2	OBMLP4 DROME	OBmlp4 drosophila
106	49	72.1	35	1	VNOB_OXYMI	P83227 oxyturanus m	179	33.5	48.3	369	1	VPE_AHSV6	OB4913 african hor
107	49	72.1	35	1	VNOB_OXYSA	P83229 oxyturanus s	180	33	48.5	1	QSBSC0 SCCHJA	OB5B0C scitrogoma	
108	49	72.1	35	1	VNOB_OXYSC	P83228 oxyturanus s	181	33	48.5	137	2	Q9TWS_CIOAB	Q9TWS cictotridium
109	49	72.1	111	1	Q4VRI2_OXYSC	Q4vri2 oxyturanus s	182	33	48.5	241	2	Q5P7A5_AZOSE	Q5p7a5 azocareus sp
110	48	70.6	38	1	DNP_DERAN	P28374 dendrocaepis s	183	33	48.5	408	2	Q8H1G9_ARATH	Q8h1g9 arabidopsis
111	48	70.6	53	2	OBGGP7_DERAN	OBGGP7 dendrocaepis s	184	33	48.5	419	2	Q9M0H3_ARATH	Q9mh3 arabidopsis
112	48	70.6	137	2	Q5Y820_XENLA	O5y820 xenopus lae	185	33	48.5	441	2	Q89RS5_BRAJA	Q89rs5 bradyrhizob
113	47	69.1	128	2	Q4T954_TERNG	Q4t954 tetraodon n	186	33	48.5	454	2	Q6MKP4_BDEBA	Q6mkp4 bdellovibri
114	47	69.1	158	1	ANFC3_FUGRO	Q805d4 fugu rubrip	187	33	48.5	472	1	E1BL_ADE41	P10546 human adeno
115	46	67.6	111	2	Q8HXV3_SAGO	Q8hxv3 saginums oe	188	33	48.5	505	2	Q7XSK0_ORYSA	Q7xsk0 oryza sativ
116	46	67.6	111	2	Q8HXV4_9PRIM	Q8hxv4 macaca sp.	189	33	48.5	539	2	Q84V17_HORVD	Q84v17 hordium vul
117	46	67.6	111	2	Q8HXV5_PONPY	Q8hxv5 pongo pygma	190	33	48.5	558	2	Q881Z0_PSEPK	Q881z0 pseudomona s
118	46	67.6	111	2	Q8HXV6_9PRIM	Q8hxv6 gorilla gor	191	33	48.5	567	2	Q8H1Z0_PALSO	Q8h1z0 palstonia s
119	46	67.6	111	2	Q8HXV7_PANTR	Q8hxv7 pan troglod	192	33	48.5	585	2	Q81B78_PLAUF	Q81b78 plasmodium
120	46	67.6	126	2	Q9D288_MOUSE	Q9d288 mus musculu	193	33	48.5	1763	2	Q4HX73_GIBZE	Q4hx73 gibberella
121	45	66.2	139	2	P79799_MICCO	P79799 micrurus co	194	33	48.5	2544	2	Q4LY33_9BURK	Q4ly33 burkholderi
122	42	61.8	740	2	Q5Z8V2_ORYSA	Q5z8v2 oryza sativ	195	33	48.5	563	2	Q5LYZ2_9TRYP	Q5lyz2 trypanosoma
123	39	57.4	33	2	Q6GUD8_FELCA	Q6gid8 felis silve	196	32.5	47.8	762	2	Q5Z8U0_ORYSA	Q5z8u0 oryza sativ
124	39	57.4	181	2	Q6TIG5_DROME	Q6tig5 drosophila	197	32.5	47.8	66	2	Q61693_CABEL	Q61693 caenorhabd
125	39	57.4	216	2	Q7SKM9_BRARE	Q7skm9 brachydanio	198	32	47.1	132	2	E1BL_ADE41	P10545 human adeno
126	38	55.9	918	2	Q4MHV9_ASPEU	Q4mhv9 aspergillus	199	32	47.1	196	1	COAE_LEPIC	Q72WV4 leptospira
127	37	54.4	407	2	Q8BET6_SHEON	Q8bet6 shewanella	200	32	47.1	196	1	COAE_LEPIC	Q7rfh9 leptospira
128	37	54.4	1067	2	Q01419_BHOMO	Q01419 bombyx mori	201	32	47.1	211	2	Q7RFH9_PLAYO	Q7rfh9 plasmodium
129	36	52.9	420	2	Q7UNAF_RHOBA	Q7una6 rhodoptirelli	202	32	47.1	233	2	Q5CLX3_SCCHJA	Q5clx3 scitrosoma
130	36	52.9	519	2	Q6NIB3_XENLA	Q6nub3 xenopus lae	203	32	47.1	260	2	Q9AAV8_ARATH	Q9AAV8 arabidopsis
131	36	52.9	541	2	Q9ZSA6_STRCO	Q9zsa6 streptomyce	204	32	47.1	262	2	Q5V399_HALMA	Q5v399 haloarcula
132	36	52.9	1076	2	Q868Q4_BOMMO	Q868q4 bombyx mori	205	32	47.1	273	2	Q5UP43_MIMIV	Q5up43 mimivirus
133	35	51.5	53	2	Q8CLV0_YERPE	Q8clv0 yersinia pe	206	32	47.1	274	2	Q9ZXA1_BPPHC	Q9zxa1 bacterioph
134	35	51.5	113	2	Q08321_YEAST	Q08321 saccharomye	207	32	47.1	280	2	Q4FKD0_9TRYP	Q4fkD0 trypanosoma
135	35	51.5	202	2	Q5AG45_CANAL	Q5ag45 candida alb	208	32	47.1	282	2	Q5AFV3_EMENT	Q5afv3 aspergillus
136	35	51.5	222	2	Q4S188_TERNG	Q4s188 tetraodon n	209	32	47.1	297	2	Q8R5M0_MOUSE	Q8r5m0 mus musculu
137	35	51.5	426	2	Q6DIC6_ERWCT	Q6dic6 erwina car	210	32	47.1	312	2	Q8TF64_HUMAN	Q8tf64 homo sapien
138	35	51.5	449	2	Q6J130_BURPS	Q6j130 burkholderi	211	32	47.1	314	2	Q4TH97_TERNG	Q4th97 tetraodon n
139	35	51.5	456	2	Q4IT19_AZCVI	Q4it19 azotobacter	212	32	47.1	347	2	Q7S227_HUMAN	Q7s227 homo sapien
140	35	51.5	487	2	Q4LKC2_9BURK	Q4lkc2 burkholderi	213	32	47.1	380	2	Q8A110_BACTN	Q8a110 bacteroides
141	35	51.5	540	2	Q82L10_STRAW	Q82l10 streptomyce	214	32	47.1	393	2	Q749J8_GEOSL	Q749j8 geobacter s
142	35	51.5	1053	2	Q8MY27_9NEOP	Q8my27 papilio xut	215	32	47.1	399	2	Q4NUU5_9M1CC	Q4nuu5 archibacte
143	35	51.5	1053	2	Q8MY35_9NEOP	Q8my35 papilio xut	216	32	47.1	405	2	Q64B02_9ARCA	Q64bc2 uncultured
144	35	51.5	1053	2	Q8MY31_9NEOP	Q8my31 papilio xut	217	32	47.1	408	2	Q8FYK9_BRUCU	Q8fyk9 bruceella su
145	35	51.5	1053	2	Q8MY33_9NEOP	Q8my33 papilio xut	218	32	47.1	410	2	Q5V6A3_HALMA	Q5v6a3 haloarcula
146	35	51.5	1336	2	Q73WQ7_MYCPA	Q73wq7 mycobacteri	219	32	47.1	411	2	Q9A961_CAVCR	Q9a961 callobacter
147	35	51.5	1351	2	Q9AV94_SOYBN	Q9av94 glycyne max	220	32	47.1	413	2	Q8R6B4_MOUSE	Q8rb64 m mus muscu
148	35	51.5	2111	1	MCAS_MYCBO	Q02251 mycobacteri	221	32	47.1	419	2	Q5R9N7_PONPY	Q5r9n7 pongo pygma
149	35	51.5	2111	1	P96291_MYCTU	P96291 mycobacteri	222	32	47.1	424	2	Q8XZ00_NITEU	Q8xz00 nitrososoma
150	35	51.5	2116	2	Q9CD78_MYCLE	Q9cd78 mycobacteri	223	32	47.1	428	2	Q5X605_LEGPA	Q5x605 legionella
151	35	51.5	2116	2	Q49624_MYCLE	Q49624 mycobacteri	224	32	47.1	428	2	Q5X605_LEGPA	Q5x605 legionella
152	35	51.5	4723	2	Q8GBA1_DROME	Q8gba1 drosophila	225	32	47.1	428	2	Q74FA3_GEOSL	Q74fa3 geobacter s
153	35	51.5	56	2	Q9FCV7_LISMO	Q9fcv7 listeria mo	226	32	47.1	428	2	Q6FRB6_ACTAD	Q6frb6 actinobact
154	34	50.0	157	2	Q5YR22_NOCFA	O5yr22 nocardia fa	227	32	47.1	431	2	Q6FRB6_ACTAD	Q6frb6 actinobact
155	34	50.0	327	2	Q9RLU1_LISMO	Q9rlu1 listeria mo	228	32	47.1	432	2	Q8R6B4_MOUSE	Q8rb64 m mus muscu
156	34	50.0	327	2	Q8Y3P8_LISMO	Q8y3p8 listeria mo	229	32	47.1	433	2	Q9N4Z0_CABEL	Q9n4z0 caenorhabd
157	34	50.0	412	2	Q513L7_ECOLI	Q513l7 escherichia	230	32	47.1	433	2	Q5YL47_SALCH	Q5yl47 salmonella
158	34	50.0	418	2	Q8TJAG_METAC	Q8tjag methanosarc	231	32	47.1	433	2	Q8ZMX1_SALTY	Q8zmx1 salmonella
159	34	50.0	446	2	Q4ZBP6_PSESY	Q4zbp6 pseudomonas	232	32	47.1	433	2	Q8Z4J3_SALTY	Q8z4j3 salmonella
160	34	50.0	446	2	Q87XK6_PSESM	Q87xk6 pseudomonas	233	32	47.1	433	2	Q5PID4_SALPA	Q5pid4 salmonella
161	34	50.0	473	2	Q78B98_9MUR1	Q78b98 rattus sp.	234	32	47.1	434	2	Q61RC8_CABER	Q61rc8 caenorhabd
162	34	50.0	479	2	Q7P2H2_FUSNV	Q7p2h2 fusobacteri	235	32	47.1	435	2	Q6FZ90_BAKOU	Q6fz90 bartonella
163	34	50.0	494	2	Q96Y04_SULTO	Q96y04 sulfolobus	236	32	47.1	436	2	Q4LK17_9BURK	Q4lk17 burkholderi
164	34	50.0	504	2	Q7DDJ1_AGRYS	Q7ddj1 agrobacteri	237	32	47.1	437	2	Q8XTN1_RALSO	Q8xtn1 ralstonia s
165	34	50.0	510	2	Q5WHS3_BACSK	Q5whs3 bacillus cl	238	32	47.1	437	2	Q9HXPS_PSEAE	Q9hxp5 pseudomonas
166	34	50.0	526	2	Q5EUT8_ORYSA	Q5eut8 oryza sativ	239	32	47.1	437	2	Q6ZH22_BURNA	Q6zh22 burkholderi
167	34	50.0	526	2	Q8H6G9_ORYSA	Q8h6g9 oryza sativ	240	32	47.1	438	2	Q86RVE_PSESM	Q86rv6 pseudomonas
168	34	50.0	536	2	Q8RSV8_FUSNN	Q8rsv8 fusobacteri	241	32	47.1	439	2	Q4L1I9_9BURK	Q4l1i9 burkholderi
169	34	50.0	648	1	FOXN1_HUMAN	O15553 homo sapien	242	32	47.1	441	2	Q8XVH5_RALSO	Q8xvh5 ralstonia s
170	34	50.0	648	1	FOXN1_MOUSE	P97715 rattus sp.	243	32	47.1	441	2	Q9BRR1_HUMAN	Q9brri homo sapien
171	34	50.0	648	2	P97715_MURRI	P97715 rattus sp.	244	32	47.1	442	2	Q88136_PSEPK	Q88136 pseudomonas
172	34	50.0	648	2	O5SYK1_MOUSE	O5syk1 mus musculu	245	32	47.1	443	2	Q91Y71_PSEPU	Q91y71 pseudomonas
173	34	50.0	829	2	Q7VZT1_PROMP	Q7vzt1 prochloroco	246	32	47.1	444	2	Q9XBD4_AKTOR	Q9xbd4 amycolatops
174	34	50.0	883	2	Q9LDG7_ARATH	Q9ldg7 arabidopsis	247	32	47.1	446	1	CITN_SALPU	P31603 salmonella
175	34	50.0	1125	2	Q54GH9_DICDI	Q54gh9 dictyosteli	248	32	47.1	446	1	CITN_SALPU	P0A250 salmonella
176	34	50.0	2108	2	Q7VER3_MYCBO	Q7ver3 mycobacteri	249	32	47.1	446	1	CITN_SALPU	P0A250 salmonella
177	34	50.0	2108	2	O53901_MYCTU	O53901 mycobacteri	250	32	47.1	446	1	CITN_SALPU	P0A250 salmonella

251	32	47.1	446	1	CITN_SALTY	P0afz8 salmonella	324	31	45.6	164	2	Q9DM95_RCMVM	Q9adw5 rat cytochrome
252	32	47.1	446	2	Q57TK4_SALCH	Q57TK4 salmonella	325	31	45.6	185	2	Q6LIC2_PHOPR	Q6LIC2 phorbacter
253	32	47.1	446	2	Q5PKT7_SALPA	Q5PKT7 salmonella	326	31	45.6	197	2	Q5I0S5_SILPO	Q5I0S5 silpobacter
254	32	47.1	447	2	Q6WSC1_PSEBL	Q6WSC1 pseudomonas	327	31	45.6	203	2	Q580E7_9TRYP	Q580E7 tryptobacter
255	32	47.1	449	2	Q6XUN5_PSESD	Q6XUN5 pseudomonas	328	31	45.6	250	2	Q7URU9_RHOBFA	Q7URU9 rhobosoma
256	32	47.1	453	2	Q8XJAO_CLOPE	Q8XJAO clostridium	329	31	45.6	260	2	Q4KG07_PSEBF5	Q4KG07 pseudomonas
257	32	47.1	456	2	Q4ZMW3_PSEBY	Q4ZMW3 pseudomonas	330	31	45.6	260	2	Q913L1_PSEAE	Q913L1 pseudomonas
258	32	47.1	457	2	Q6LRW7_CAEER	Q6LRW7 caenorhabditis	331	31	45.6	260	2	Q89R43_BRJJA	Q89R43 bradyrhizobium
259	32	47.1	458	2	Q16700_CAEEL	Q16700 caenorhabditis	332	31	45.6	269	2	Q4LLQ1_9BRK	Q4LLQ1 bradyrhizobium
260	32	47.1	459	2	Q9HTR6_THEAC	Q9HTR6 thermoplasma	333	31	45.6	274	2	Q859B1_9CAUD	Q859B1 bacteriophage
261	32	47.1	461	2	Q8JJC1_SERMA	Q8JJC1 serratia	334	31	45.6	286	2	Q8YJ90_BRJJA	Q8YJ90 bradyrhizobium
262	32	47.1	462	2	Q9HWG1_PSEAE	Q9HWG1 pseudomonas	335	31	45.6	301	2	Q8JUR0_PSEAE	Q8JUR0 pseudomonas
263	32	47.1	463	2	Q9H9P8_HUMAN	Q9H9P8 homo sapiens	336	31	45.6	308	2	Q8JUM6_9BROM	Q8JUM6 spring bean
264	32	47.1	464	2	Q68BY0_RHOSR	Q68BY0 rhodococcus	337	31	45.6	319	2	Q9R187_STRCO	Q9R187 streptomyces
265	32	47.1	464	2	Q6REL7_9NOCA	Q6REL7 rhodococcus	338	31	45.6	352	2	Q5V497_HALMA	Q5V497 haloarcula
266	32	47.1	464	2	Q5YUE1_NOCFA	Q5YUE1 nocardia	339	31	45.6	353	1	ISFG_GEOSL	Q7ad60 geobacter
267	32	47.1	464	2	Q9IYPO_MOUSE	Q9IYPO mus musculus	340	31	45.6	356	2	Q4SADI_TETNG	Q4SADI tetrarodon
268	32	47.1	467	2	Q8VUZ0_9BRAD	Q8VUZ0 bradyrhizobium	341	31	45.6	367	2	Q4IYB_GIBZE	Q4IYB gibberella
269	32	47.1	467	2	Q73LY1_TREDE	Q73LY1 treponema	342	31	45.6	369	2	Q8UGL7_AGRF5	Q8UGL7 agrobacterium
270	32	47.1	467	2	Q5P152_AZOSE	Q5P152 azorhizobium	343	31	45.6	377	2	Q61XK9_CAEER	Q61XK9 caenorhabditis
271	32	47.1	470	2	Q8COSO_MOUSE	Q8COSO mus musculus	344	31	45.6	381	2	Q8TUA7_METAC	Q8TUA7 methanobacterium
272	32	47.1	488	2	Q97YU3_SUISO	Q97YU3 sulfobolus	345	31	45.6	386	2	Q8PYZ5_METWA	Q8PYZ5 methanobacterium
273	32	47.1	492	2	Q4U455_POLCB	Q4U455 polyangium	346	31	45.6	387	2	Q9HMR5_HALSA	Q9HMR5 halobacterium
274	32	47.1	493	2	Q4KMR2_PSEBF5	Q4KMR2 pseudomonas	347	31	45.6	391	2	Q98MV7_RHILIO	Q98MV7 rhizobium
275	32	47.1	509	1	ZKRI_CHICK	P30373 gallus galli	348	31	45.6	392	2	Q4SEF5_TETNG	Q4SEF5 tetrarodon
276	32	47.1	510	2	Q4SCN6_TETNG	Q4SCN6 tetrarodon	349	31	45.6	392	2	Q9SYD6_CAEEL	Q9SYD6 caenorhabditis
277	32	47.1	512	2	Q53K43_ORYSA	Q53K43 oryza sativa	350	31	45.6	394	2	Q60BA8_METCA	Q60BA8 methanobacterium
278	32	47.1	514	1	TBLIR_HUMAN	Q9bdk7 homo sapiens	351	31	45.6	398	2	Q5KUB8_GEOKA	Q5KUB8 geobacterium
279	32	47.1	514	1	TBLIR_MOUSE	Q9bdk7 mus musculus	352	31	45.6	400	1	YCEI_BACSU	Q34691 bacillus subtilis
280	32	47.1	519	2	Q9SD16_ARATH	Q9SD16 arabidopsis	353	31	45.6	403	2	Q6SM62_MANSM	Q6SM62 manihottia
281	32	47.1	519	2	Q7SZM9_XENILA	Q7SZM9 xenopus	354	31	45.6	405	2	Q8ENB2_OCEIH	Q8ENB2 ocellularia
282	32	47.1	522	2	Q6GPC6_XENILA	Q6GPC6 xenopus	355	31	45.6	405	2	Y8NE2_PASMU	Y8NE2 pseudomonas
283	32	47.1	524	2	Q8S220_ORYSA	Q8S220 oryza sativa	356	31	45.6	407	1	Y1104_HAETN	Y1104 haemophilus
284	32	47.1	529	2	Q84WU7_ARATH	Q84WU7 arabidopsis	357	31	45.6	408	2	Q57B29_BRUBAB	Q57B29 brucella
285	32	47.1	541	2	Q6NV16_BRARE	Q6NV16 brachydanio	358	31	45.6	411	1	AATC_CHICK	P00504 gallus galli
286	32	47.1	552	2	Q6ZMH3_BURMA	Q6ZMH3 burkholderia	359	31	45.6	415	2	Q4LUG3_9BURK	Q4LUG3 burkholderia
287	32	47.1	556	2	Q6JMW8_BURPS	Q6JMW8 burkholderia	360	31	45.6	415	2	Q8DX01_STRAS	Q8DX01 streptococcus
288	32	47.1	558	2	Q7MKN2_BORBR	Q7MKN2 bordetella	361	31	45.6	415	2	Q8E2V1_STRAS	Q8E2V1 streptococcus
289	32	47.1	558	2	Q7W796_BORBR	Q7W796 bordetella	362	31	45.6	417	2	Q8YR81_METKA	Q8YR81 methanopyrus
290	32	47.1	558	2	Q7VVT8_BORBR	Q7VVT8 bordetella	363	31	45.6	418	2	Q8XRNA_RALSO	Q8XRNA ralsostonia
291	32	47.1	562	2	Q84PV5_ORYSA	Q84PV5 oryza sativa	364	31	45.6	419	2	Q9VDU8_DROME	Q9VDU8 dirosophila
292	32	47.1	565	2	Q5T230_BRARE	Q5T230 brachydanio	365	31	45.6	426	2	Q4J7U1_SULAC	Q4J7U1 sulfolobus
293	32	47.1	565	2	Q7ZTC0_BRARE	Q7ZTC0 brachydanio	366	31	45.6	426	2	Q4LOF6_9BURK	Q4LOF6 burkholderia
294	32	47.1	566	1	YCD6_YEAST	P25370 saccharomyces	367	31	45.6	428	2	Q4ZRC6_PSEBY	Q4ZRC6 pseudomonas
295	32	47.1	570	2	Q7NY54_CHRVO	Q7NY54 chromobacterium	368	31	45.6	429	2	Q5Z000_PSEPU	Q5Z000 pseudomonas
296	32	47.1	579	2	Q7UX97_RHOBFA	Q7UX97 rhodospirillum	369	31	45.6	429	2	Q9WWE2_PSEPU	Q9WWE2 pseudomonas
297	32	47.1	580	2	Q4SP82_TETNG	Q4SP82 tetrarodon	370	31	45.6	429	2	Q8BNJ8_PSEBP	Q8BNJ8 pseudomonas
298	32	47.1	625	2	Q8B282_MOUSE	Q8B282 mus musculus	371	31	45.6	430	2	Q5TSC8_SALCH	Q5TSC8 salmonella
299	32	47.1	625	2	Q5FMX9_MOUSE	Q5FMX9 mus musculus	372	31	45.6	431	2	Q6RBB5_SODGL	Q6RBB5 sodalite
300	32	47.1	663	2	Q5BAD7_EMBENI	Q5BAD7 aspergillus	373	31	45.6	432	2	Q91609_PSEAE	Q91609 pseudomonas
301	32	47.1	689	2	Q5EC47_RAT	Q5EC47 rattus norvegicus	374	31	45.6	433	2	Q4ZP82_PSEBY	Q4ZP82 pseudomonas
302	32	47.1	742	2	Q5LFO3_BACFN	Q5LFO3 bacteroides	375	31	45.6	433	2	Q5YUM8_NOCFA	Q5YUM8 nocardia
303	32	47.1	742	2	Q64MN8_BACFR	Q64MN8 bacteroides	376	31	45.6	433	2	Q8YX82_PSEBM	Q8YX82 pseudomonas
304	32	47.1	796	2	Q4IBG6_GIBZE	Q4IBG6 gibberella	377	31	45.6	435	2	Q7NZC9_CHRVO	Q7NZC9 chromobacterium
305	32	47.1	876	2	Q6CNT2_KLUIA	Q6CNT2 kluyveromyces	378	31	45.6	437	2	Q7M899_WOLSU	Q7M899 wolinella
306	32	47.1	876	2	Q7SHH6_NEUICR	Q7SHH6 neurospora	379	31	45.6	439	2	Q6ZAY1_BURMA	Q6ZAY1 burkholderia
307	32	47.1	1180	2	Q9N583_CAEEL	Q9N583 caenorhabditis	380	31	45.6	440	2	Q63K08_BURPS	Q63K08 burkholderia
308	32	47.1	1758	2	Q95Y84_CAEEL	Q95Y84 caenorhabditis	381	31	45.6	440	2	Q8S7W1_ORYSA	Q8S7W1 oryza sativa
309	32	47.1	1871	2	Q9Z5K6_MYCLE	Q9Z5K6 mycobacterium	382	31	45.6	440	2	Q6TMA4_9NOCA	Q6TMA4 rhodococcus
310	31.5	46.3	315	2	Q8H9W4_9CAUD	Q8H9W4 pseudomonas	383	31	45.6	441	2	Q5YRL6_NOCFA	Q5YRL6 nocardia
311	31.5	46.3	315	2	Q9F696_BARBA	Q9F696 bartonella	384	31	45.6	443	2	Q4FL43_9RICK	Q4FL43 rickettsia
312	31.5	46.3	737	2	Q4SZD1_TETNG	Q4SZD1 tetrarodon	385	31	45.6	449	2	Q8ZRC8_SALTY	Q8ZRC8 salmonella
313	31	45.6	56	2	Q54UT2_DICDI	Q54UT2 dictyostelium	386	31	45.6	450	2	Q92YS3_RHIME	Q92YS3 rhizobium
314	31	45.6	69	2	Q11044_SCYCA	Q11044 scyllorhinus	387	31	45.6	454	1	YAJR_ECOLI	YAJR escherichia
315	31	45.6	83	2	Q6TGR3_PYTMO	Q6TGR3 pythium	388	31	45.6	454	2	Q5PFQ3_SALPA	Q5PFQ3 salmonella
316	31	45.6	85	2	Q67VG7_ORYSA	Q67VG7 oryza sativa	389	31	45.6	454	2	Q8ZAY2_YERPE	Q8ZAY2 yerkesia
317	31	45.6	108	2	Q4FRR6_9GAMM	Q4FRR6 psychrobacter	390	31	45.6	454	2	Q8Z8W1_SALTI	Q8Z8W1 salmonella
318	31	45.6	112	2	Q4RRD3_TETNG	Q4RRD3 tetrarodon	391	31	45.6	454	2	Q665D6_YERPS	Q665D6 yerkesia
319	31	45.6	132	2	Q01642_DRGGR	Q01642 dirosophila	392	31	45.6	454	2	Q6D837_ERWCT	Q6D837 erwinia
320	31	45.6	142	2	Q8GVX8_ORYSA	Q8GVX8 oryza sativa	393	31	45.6	456	2	Q8ZCS3_YERPS	Q8ZCS3 yerkesia
321	31	45.6	144	2	Q5B205_SCHJA	Q5B205 schistosoma	394	31	45.6	456	2	Q66DU6_YERPS	Q66DU6 yerkesia
322	31	45.6	158	2	Q74DH7_GEOSL	Q74DH7 geobacter	395	31	45.6	456	2	Q8XET1_ECHER	Q8XET1 escherichia
323	31	45.6	164	2	Q93CZ0_LACSK	Q93CZ0 lactobacillus	396	31	45.6	458	2	Q4ZUFO_PSEBY	Q4ZUFO pseudomonas

397	31	45.6	458	2	083BP3_COXBU	083BP3_coxiella bu	470	31	45.6	2073	2	073Yt8_MYCPA	073Yt8_mycobacteri
398	31	45.6	460	2	P70737_ALCEU	P70737 alcaligenes	471	31	45.6	2085	2	07U0G2_MYCBO	07U0G2_mycobacteri
399	31	45.6	462	2	07PC06_RICSI	07PC06 rickettsia	472	31	45.6	2101	2	08YK52_MYCTU	08YK52_mycobacteri
400	31	45.6	462	2	05LCJ8_BACFN	05LCJ8 bacteroides	473	31	45.6	2138	2	08N6C0_HUMAN	08N6C0_homo sapien
401	31	45.6	462	2	089ZJ8_BACTN	089ZJ8 bacteroides	474	31	45.6	2144	2	04VM19_HUMAN	04VM19_homo sapien
402	31	45.6	462	2	092HW3_RICCN	092HW3 rickettsia	475	31	45.6	2157	2	04VM18_HUMAN	04VM18_homo sapien
403	31	45.6	462	2	064XEL_BACPR	064XEL bacteroides	476	31	45.6	2179	2	04VM17_HUMAN	04VM17_homo sapien
404	31	45.6	463	2	06CHP7_ALDCE	06CHP7 alcaligenes	477	31	45.6	2221	1	CAC1C_HUMAN	013936_homo sapien
405	31	45.6	463	2	09RHQ1_VAPRD	09RHQ1 varioloxax	478	478	44.9	292	2	04NX98_9DELT	04NX98_aeromonas
406	31	45.6	463	2	08KN29_COMAC	08KN29 commonas a	479	30.5	389	2	06AU05_DESPS	06AU05_desulfoale	
407	31	45.6	463	2	0931J3_BURCE	0931J3 burkholderi	480	30	44.1	41	2	07QW05_GIALA	07QW05_giardia lam
408	31	45.6	464	2	04ZMS3_PSESY	04ZMS3 pseudomonas	481	30	44.1	89	2	07J138_TREDE	07J138_treponema d
409	31	45.6	464	2	04K562_PSEPS	04K562 pseudomonas	482	30	44.1	94	2	08BN69_MOUSE	08BN69_mus musculi
410	31	45.6	464	2	0880K6_PSEPK	0880K6 pseudomonas	483	30	44.1	113	2	09WHJ5_PLAFA	09WHJ5_plasmodium
411	31	45.6	464	2	05HRH0_STABQ	05HRH0 staphylococ	484	30	44.1	120	1	ARD2_ECOLI	P52148 escherichia
412	31	45.6	464	2	0889U2_PSESM	0889U2 pseudomonas	485	30	44.1	120	2	0943Y7_9POLA	0943Y7_inco plasm
413	31	45.6	466	2	04V5J2_DROME	04V5J2 drosoephila	486	30	44.1	125	2	07R6N9_GIALA	07R6N9_giardia lam
414	31	45.6	468	1	LEU2_HAEIN	P49668 haemophilus	487	30	44.1	126	2	0913Z1_PSEAE	0913Z1_pseudomonas
415	31	45.6	468	2	04OL52_HAE18	04OL52 haemophilus	488	30	44.1	137	2	0130J2_BRARE	0130J2_brechrantio
416	31	45.6	469	2	065V07_MANSM	065V07 manthelamia	489	30	44.1	142	2	04ZX16_PSESY	04ZX16_pseudomonas
417	31	45.6	474	2	09HK33_THEAC	09HK33 thermoplaam	490	30	44.1	145	2	065D89_BACLD	065D89_bacillus i
418	31	45.6	479	2	0649M0_GARCH	0649M0 uncultured	491	30	44.1	146	2	062NRS_BACLD	062NRS_bacillus i
419	31	45.6	479	2	064A50_GARCH	064A50 uncultured	492	30	44.1	154	2	0755Z1_ASHGO	0755Z1_ashya goss
420	31	45.6	479	2	064ED3_GARCH	064ED3 uncultured	493	30	44.1	155	2	091963_AARPE	091963_aeropyrum p
421	31	45.6	480	2	0978M4_THEVO	0978M4 thermoplaam	494	30	44.1	172	2	061W18_SALPU	061W18_salmoneila
422	31	45.6	482	2	094305_CABEL	094305 caenorhabdi	495	30	44.1	173	2	05TRX2_HUMAN	05TRX2_homo sapien
423	31	45.6	486	2	09HLK4_THEAC	09HLK4 thermoplaam	496	30	44.1	178	2	05H782_STEAT	05H782_streptomyc
424	31	45.6	488	2	05LYE9_STR11	05LYE9 streptococc	497	30	44.1	188	2	04PL94_ARATH	04PL94_arabidopsis
425	31	45.6	488	2	05M312_STR12	05M312 streptococc	498	30	44.1	195	2	058FV5_ARATH	058FV5_arabidopsis
426	31	45.6	495	2	08Z0D2_ANASP	08Z0D2 anaena sp	499	30	44.1	214	2	084RK0_ARATH	084RK0_arabidopsis
427	31	45.6	498	2	04Y895_PLACH	04Y895 plasmodium	500	30	44.1	214	2	Y315_TREPA	P56822 treponema p
428	31	45.6	503	2	06A679_PROAC	06A679 propionibac	501	30	44.1	215	1	080LX0_GINFA	080LX0_ginfa
429	31	45.6	505	2	061I87_DROME	061I87 drosoephila	502	30	44.1	220	2	0601T5_VIRU	0601T5_virus
430	31	45.6	511	2	0529L9_MAGGR	0529L9 magnaporth	503	30	44.1	222	2	072WV7_DESVI	072WV7_deesulfole
431	31	45.6	512	2	07RJQ3_PLAYO	07RJQ3 plasmodium	504	30	44.1	222	2	0840V2_SPHEL	0840V2_sphingomona
432	31	45.6	518	2	04IWN9_AZOV1	04IWN9 azocobacter	505	30	44.1	235	2	075GDO_ORYSA	075GDO_oryza sativ
433	31	45.6	520	2	08FKB4_ECOL6	08FKB4 escherichia	506	30	44.1	239	2	080LW8_GINFA	080LW8_ginfa
434	31	45.6	521	2	08X1F6_GLOIN	08X1F6 glomus intr	507	30	44.1	239	2	04WM25_ASFPU	04WM25_aspergillus
435	31	45.6	522	1	TBL1Y_HUMAN	09Bd87 homo sapien	508	30	44.1	246	2	059W69_CANAL	059W69_candida alb
436	31	45.6	526	1	TBL1X_HUMAN	060907 homo sapien	509	30	44.1	249	2	SFSA_PROMM	074Vc9_pichloroco
437	31	45.6	527	1	TBL1X_MOUSE	09QX67 mus musculi	510	30	44.1	251	1	VMT1_IAPPR	P03488 influenza a
438	31	45.6	527	2	08AVI6_HORVD	08AVI6 hordeum vul	511	30	44.1	252	1	06E406_GINFA	06E406_influenza a
439	31	45.6	532	2	09S735_ARATH	09S735 arabidopsis	512	30	44.1	252	2	077MI3_GINFA	077MI3_influenza a
440	31	45.6	532	2	089SV9_BRATA	089SV9 braehyrizob	513	30	44.1	252	2	077W51_GINFA	077W51_influenza a
441	31	45.6	534	2	07NHY5_CHRYO	07NHY5 chromocacce	514	30	44.1	252	2	07TGUV_GINFA	07TGUV_influenza a
442	31	45.6	538	2	09VDV7_DROME	09VDV7 drosoephila	515	30	44.1	252	2	077GUV_GINFA	077GUV_influenza a
443	31	45.6	540	2	059F53_HUMAN	059F53 homo sapien	516	30	44.1	252	2	0807V4_GINFA	0807V4_influenza a
444	31	45.6	544	2	04S0B6_TENNG	04S0B6 tetraodon n	517	30	44.1	252	2	0807V5_GINFA	0807V5_influenza a
445	31	45.6	549	2	08H6G6_ORYSA	08H6G6 oryza sativ	518	30	44.1	252	2	0807V7_GINFA	0807V7_influenza a
446	31	45.6	552	2	069794_ORYSA	069794 oryza sativ	519	30	44.1	252	2	0807V8_GINFA	0807V8_influenza a
447	31	45.6	562	2	08Z0B1_PYRAE	08Z0B1 pyrobaculum	520	30	44.1	252	2	0809Y3_GINFA	0809Y3_influenza a
448	31	45.6	563	2	04S705_TENNG	04S705 tetraodon n	521	30	44.1	252	2	0809Y5_GINFA	0809Y5_influenza a
449	31	45.6	566	2	04W9V3_ASFPU	04W9V3 aspergillus	522	30	44.1	252	2	0809Y9_GINFA	0809Y9_influenza a
450	31	45.6	568	2	0814W7_PLAF7	0814W7 plasmodium	523	30	44.1	252	2	0809Z5_GINFA	0809Z5_influenza a
451	31	45.6	569	2	04R8H1_MACPA	04R8H1 macaca fasc	524	30	44.1	252	2	0809Z7_GINFA	0809Z7_influenza a
452	31	45.6	582	2	08H6G7_ORYSA	08H6G7 oryza sativ	525	30	44.1	252	2	0809Z8_GINFA	0809Z8_influenza a
453	31	45.6	584	2	04FY0Y_9GAMM	04FY0Y psychrobact	526	30	44.1	252	2	080A03_GINFA	080A03_influenza a
454	31	45.6	695	2	063PL9_BURPS	063PL9 burkholderi	527	30	44.1	252	2	080A04_GINFA	080A04_influenza a
455	31	45.6	700	2	062FM2_BURMA	062FM2 burkholderi	528	30	44.1	252	2	080A07_GINFA	080A07_influenza a
456	31	45.6	720	2	0548Q1_DICDI	0548Q1 dictyosteli	529	30	44.1	252	2	080FU1_GINFA	080FU1_influenza a
457	31	45.6	722	1	PATY_CITLI	042667 citrus limo	530	30	44.1	252	2	080FU3_GINFA	080FU3_influenza a
458	31	45.6	725	2	054R45_DICDI	054R45 dictyosteli	531	30	44.1	252	2	080FU5_GINFA	080FU5_influenza a
459	31	45.6	744	2	05BET2_EMENT	05BET2 aspergillus	532	30	44.1	252	2	080FU7_GINFA	080FU7_influenza a
460	31	45.6	782	2	051YAI_MAGGR	051YAI magnaporth	533	30	44.1	252	2	080FU9_GINFA	080FU9_influenza a
461	31	45.6	805	2	04R7B6_MACPA	04R7B6 macaca fasc	534	30	44.1	252	2	080FV3_GINFA	080FV3_influenza a
462	31	45.6	825	2	08A2K5_BACTN	08A2K5 bacteroides	535	30	44.1	252	2	080FV5_GINFA	080FV5_influenza a
463	31	45.6	839	2	0606V3_METCA	0606V3 methylcocc	536	30	44.1	252	2	080FW1_GINFA	080FW1_influenza a
464	31	45.6	872	2	08YTT7_ANASP	08YTT7 anabaena sp	537	30	44.1	252	2	080FW3_GINFA	080FW3_influenza a
465	31	45.6	1184	2	06B008_DEBHA	06B008 debaryomyce	538	30	44.1	252	2	080FW5_GINFA	080FW5_influenza a
466	31	45.6	1219	2	04P4I8_USITMA	04P4I8 ussiliago ma	539	30	44.1	252	2	080FW7_GINFA	080FW7_influenza a
467	31	45.6	1582	2	050437_MYCTU	050437 mycobacteri	540	30	44.1	252	2	080FW9_GINFA	080FW9_influenza a
468	31	45.6	1890	2	049528_ARATH	049528 arabidopsis	541	30	44.1	252	2	080FX1_GINFA	080FX1_influenza a
469	31	45.6	2028	2	Q5XPX0_ARATH	Q5XPX0 arabidopsis	542	30	44.1	252	2	080FX1_GINFA	080FX1_influenza a

543	30	44.1	252	2	Q80FX3_9INFA	Q80FX3_influenza a	616	30	44.1	384	2	Q54QNT_DICDI	Q54QNT_dicystosteli
544	30	44.1	252	2	Q80FX5_9INFA	Q80FX5_influenza a	617	30	44.1	384	2	Q4NRC7_9EBLT	Q4NRC7_aeromyxob
545	30	44.1	252	2	Q80FX7_9INFA	Q80FX7_influenza a	618	30	44.1	384	2	Q501OC_XENLA	Q501OC_xenopus lae
546	30	44.1	252	2	Q80FX9_9INFA	Q80FX9_influenza a	619	30	44.1	393	2	Q9W562_ORYSA	Q9W562_oryza sativ
547	30	44.1	252	2	Q80FY1_9INFA	Q80FY1_influenza a	620	30	44.1	395	2	Q4U9C7_SULAC	Q4U9C7_sulfolobus
548	30	44.1	252	2	Q80FY3_9INFA	Q80FY3_influenza a	621	30	44.1	398	1	Y1317_METUA	Y1317_methanococ
549	30	44.1	252	2	Q80FY7_9INFA	Q80FY7_influenza a	622	30	44.1	398	2	Q6HIS7_BACHK	Q6HIS7_bacillus th
550	30	44.1	252	2	Q80FZ1_9INFA	Q80FZ1_influenza a	623	30	44.1	399	2	Q9ZFP5_SALTY	Q9ZFP5_salmomella
551	30	44.1	252	2	Q80FZ3_9INFA	Q80FZ3_influenza a	624	30	44.1	399	2	Q4MLT2_BACCE	Q4MLT2_bacillus ce
552	30	44.1	252	2	Q80FZ5_9INFA	Q80FZ5_influenza a	625	30	44.1	399	2	Q72X31_BACCR	Q72X31_bacillus ce
553	30	44.1	252	2	Q80FZ7_9INFA	Q80FZ7_influenza a	626	30	44.1	399	2	Q814L1_BACCR	Q814L1_bacillus ce
554	30	44.1	252	2	Q80G29_9INFA	Q80G29_influenza a	627	30	44.1	399	2	Q81UN5_BACAN	Q81UN5_bacillus an
555	30	44.1	252	2	Q80G01_9INFA	Q80G01_influenza a	628	30	44.1	399	2	Q6HAL8_BACHK	Q6HAL8_bacillus th
556	30	44.1	252	2	Q80G03_9INFA	Q80G03_influenza a	629	30	44.1	399	2	Q9ZM18_RHIME	Q9ZM18_rhizobium m
557	30	44.1	252	2	Q80G05_9INFA	Q80G05_influenza a	630	30	44.1	399	2	Q63013_BACCC	Q63013_bacillus ce
558	30	44.1	252	2	Q80G07_9INFA	Q80G07_influenza a	631	30	44.1	400	2	Q63B83_BACCC	Q63B83_bacillus ce
559	30	44.1	252	2	Q80G09_9INFA	Q80G09_influenza a	632	30	44.1	400	2	Q65MD9_BACLD	Q65MD9_bacillus l1
560	30	44.1	252	2	Q80G11_9INFA	Q80G11_influenza a	633	30	44.1	404	2	Q6RGG1_ECOLD	Q6RGG1_escherichia
561	30	44.1	252	2	Q80G13_9INFA	Q80G13_influenza a	634	30	44.1	404	2	Q6RGG2_ECOLD	Q6RGG2_escherichia
562	30	44.1	252	2	Q80LX2_9INFA	Q80LX2_influenza a	635	30	44.1	404	2	Q7B0V2_SALTY	Q7B0V2_salmomella
563	30	44.1	252	2	Q91GM3_9INFA	Q91GM3_influenza a	636	30	44.1	404	2	Q7BL41_SALET	Q7BL41_salmomella
564	30	44.1	252	2	Q91GM8_9INFA	Q91GM8_influenza a	637	30	44.1	404	2	Q8GU08_ECOLD	Q8GU08_escherichia
565	30	44.1	252	2	Q91GN4_9INFA	Q91GN4_influenza a	638	30	44.1	404	2	Q8VW40_KLEPN	Q8VW40_klebsiella
566	30	44.1	252	2	Q92PFO_9INFA	Q92PFO_influenza a	639	30	44.1	404	2	Q5BXN3_VIBCH	Q5BXN3_vibrio chol
567	30	44.1	252	2	Q90QNS_9INFA	Q90QNS_influenza a	640	30	44.1	404	2	Q9FOD3_ECOLD	Q9FOD3_escherichia
568	30	44.1	252	2	Q9WB34_9INFA	Q9WB34_influenza a	641	30	44.1	404	2	Q9F8W2_ECOLD	Q9F8W2_escherichia
569	30	44.1	252	2	Q9WB28_9INFA	Q9WB28_influenza a	642	30	44.1	404	2	Q9S6C3_SALTY	Q9S6C3_salmomella
570	30	44.1	252	2	Q9WB22_9INFA	Q9WB22_influenza a	643	30	44.1	404	2	Q9ZHH4_SALTY	Q9ZHH4_salmomella
571	30	44.1	252	2	Q9WB24_9INFA	Q9WB24_influenza a	644	30	44.1	404	2	Q50176_PASMU	Q50176_pasteurella
572	30	44.1	252	2	Q9WB26_9INFA	Q9WB26_influenza a	645	30	44.1	404	2	Q8VWNO_VIBCH	Q8VWNO_vibrio chol
573	30	44.1	253	2	Q5TRX3_HUMAN	Q5TRX3_homo sapien	646	30	44.1	406	1	FAB8_BUCAI	FAB8_buchnera ap
574	30	44.1	254	2	Q5LUB1_SILPO	Q5LUB1_silicibacte	647	30	44.1	408	2	Q5NO1O_ANGOA	Q5NO1O_anopheles g
575	30	44.1	254	2	Q5FPP0_GLUXO	Q5FPP0_gliconobact	648	30	44.1	409	2	Q9SUS8_ARATH	Q9SUS8_arabidopsis
576	30	44.1	258	2	Q92TW8_RHIME	Q92TW8_rhizobium m	649	30	44.1	412	2	Q81228_ENTFA	Q81228_entreroceccu
577	30	44.1	264	2	Q9UTP5_SCHPO	Q9UTP5_schizosacch	650	30	44.1	414	2	Q7U8H8_SYNPX	Q7U8H8_synechococc
578	30	44.1	265	2	Q9MSK0_ORYSA	Q9MSK0_oryza sativ	651	30	44.1	414	2	Q9ZU74_RHIME	Q9ZU74_rhizobium m
579	30	44.1	270	1	Y619_TREPA	Y61928_trepomona p	652	30	44.1	417	1	TNR25_HUMAN	TNR25_h tumor nec
580	30	44.1	276	2	Q4PLS5_ARATH	Q4PLS5_arabidopsis	653	30	44.1	417	2	Q5TRX5_HUMAN	Q5TRX5_homo sapien
581	30	44.1	277	2	Q5TRX4_HUMAN	Q5TRX4_homo sapien	654	30	44.1	417	2	Q81F45_ARATH	Q81F45_arabidopsis
582	30	44.1	284	2	Q8W0R5_SORBI	Q8W0R5_sorghum bic	655	30	44.1	418	2	Q976U9_SULTO	Q976U9_sulfolobus
583	30	44.1	291	2	Q5C214_CRYPV	Q5C214_cryptospori	656	30	44.1	418	2	Q5TRX7_HUMAN	Q5TRX7_homo sapien
584	30	44.1	291	2	Q5CNF6_CRYHO	Q5CNF6_cryptospori	657	30	44.1	418	2	Q5OLG3_ORYSA	Q5OLG3_oryza sativ
585	30	44.1	292	2	Q9U231_CABEL	Q9U231_caenorhabdi	658	30	44.1	420	2	Q6ZB40_BURMA	Q6ZB40_burkholderi
586	30	44.1	297	2	Q5NR91_ZYMOA	Q5NR91_zymomonas m	659	30	44.1	421	2	Q8RW9P_ARATH	Q8RW9P_arabidopsis
587	30	44.1	304	2	Q8XLA4_CLOPE	Q8XLA4_clostridium	660	30	44.1	422	2	Q9L125_STRCO	Q9L125_streptomyce
588	30	44.1	307	2	Q8YMW2_ANKSP	Q8YMW2_anabaena sp	661	30	44.1	426	2	Q81BXS_HUMAN	Q81BXS_homo sapien
589	30	44.1	310	2	Q85YJ3_DROME	Q85YJ3_drosophila	662	30	44.1	427	1	YDFJ_ECOLD	YDFJ_escherichia
590	30	44.1	310	2	Q5BKW9_BRARE	Q5BKW9_brachydanio	663	30	44.1	427	2	Q7ADX7_ECOS7	Q7ADX7_ectocorys
591	30	44.1	320	2	Q52085_POLPA	Q52085_polysphondy	664	30	44.1	427	2	Q63UC9_BURPS	Q63UC9_burkholderi
592	30	44.1	321	2	Q4FEI7_PLAMG	Q4FEI7_pliococsten	665	30	44.1	427	2	Q8XB44_ECOS7	Q8XB44_escherichia
593	30	44.1	325	1	Q8ZPI9_SALTY	Q8ZPI9_salmomella	666	30	44.1	429	2	Q96XE1_SULTO	Q96XE1_sulfolobus
594	30	44.1	328	1	GPW6B_MOUSE	GP3803_mus musculus	667	30	44.1	429	2	Q970Z3_ARATH	Q970Z3_arabidopsis
595	30	44.1	333	2	Q949H8_FESPR	Q949H8_festuca pra	668	30	44.1	431	2	Q5KYJ3_GEOKA	Q5KYJ3_geobacillus
596	30	44.1	339	2	Q5BAJ1_EMBENI	Q5BAJ1_aspergillus	669	30	44.1	431	2	Q6SIV8_BACLD	Q6SIV8_bacillus l1
597	30	44.1	349	2	Q6ZN88_HUMAN	Q6ZN88_homo sapien	670	30	44.1	433	2	Q83O87_SHIFL	Q83O87_shigella fl
598	30	44.1	350	2	Q7KPA7_LOCOMI	Q7KPA7_locusta mig	671	30	44.1	435	2	Q97CN2_THIEVO	Q97CN2_thermoplasm
599	30	44.1	353	1	YKFI_YEAST	YK5713_saccharomyc	672	30	44.1	435	2	Q4LNM8_9BURK	Q4LNM8_burkholderi
600	30	44.1	354	1	CADH1_EUCGU	Q42126_eucalyptus	673	30	44.1	436	2	Q4LNM3_9BURK	Q4LNM3_burkholderi
601	30	44.1	355	1	CADH1_EUCBO	P50746_eucalyptus	674	30	44.1	436	2	Q6F8A9_ACITAD	Q6F8A9_acinetobact
602	30	44.1	356	1	CADH2_EUCGU	P31655_eucalyptus	675	30	44.1	436	2	Q92NM2_RHIME	Q92NM2_rhizobium m
603	30	44.1	356	1	CADH_EUCGL	Q64969_eucalyptus	676	30	44.1	437	2	Q4K948_PSEPS	Q4K948_pseudomonas
604	30	44.1	356	2	Q9FUNG_9MYRT	Q9FUNG_eucalyptus	677	30	44.1	437	2	Q6ZHP0_BURMA	Q6ZHP0_burkholderi
605	30	44.1	357	2	Q59902_EMENT	Q59902_emeritella	678	30	44.1	437	2	Q63W18_BURPS	Q63W18_burkholderi
606	30	44.1	358	2	Q6GUH8_MAIZE	Q6GUH8_zea mays (m	679	30	44.1	438	2	Q63NM7_BURPS	Q63NM7_burkholderi
607	30	44.1	359	2	Q96558_LOCOMI	Q96558_locusta mig	680	30	44.1	443	2	Q4U3T2_AZOVI	Q4U3T2_azotobacter
608	30	44.1	366	2	Q95YQ1_ARATH	Q95YQ1_arabidopsis	681	30	44.1	443	2	Q5YTV0_NOCFA	Q5YTV0_nocardiella fa
609	30	44.1	369	2	Q525R9_MAGGR	Q525R9_magnaporthe	682	30	44.1	444	2	Q63KM1_BURPS	Q63KM1_burkholderi
610	30	44.1	374	2	Q53019_PASPI	Q53019_pasteurella	683	30	44.1	444	2	Q62C15_BURMA	Q62C15_burkholderi
611	30	44.1	376	2	Q4U874_SULAC	Q4U874_sulfolobus	684	30	44.1	444	2	Q62DQ2_BURMA	Q62DQ2_burkholderi
612	30	44.1	376	2	Q413M7_GIBZE	Q413M7_gibberella	685	30	44.1	444	2	Q631FO_BURPS	Q631FO_burkholderi
613	30	44.1	379	2	Q5YPU6_NOCFA	Q5YPU6_nocardiella fa	686	30	44.1	445	2	Q4ZUV7_PSESY	Q4ZUV7_pseudomonas
614	30	44.1	383	2	Q7QBEM_ANGOA	Q7QBEM_anopheles g	687	30	44.1	445	2	Q87YJ5_PESBM	Q87YJ5_pseudomonas
615	30	44.1	384	2	Q8ZVE1_PYRAE	Q8ZVE1_pyrobaculum	688	30	44.1	445	2		

689	30	44.1	446	2	09HLT4_THRAC	09hlt4	thermoplaam	762	30	44.1	585	2	04GZ72_9TRYP	04gz72	trypanosoma
690	30	44.1	446	2	05B4D0_9TRYP	05b4d0	trypanosoma	763	30	44.1	586	2	04SD07_TESTNG	04sd07	tetradion n
691	30	44.1	446	2	07M5L6_BORPA	07m5l6	botdeiteila	764	30	44.1	611	2	06RUM3_BRARE	06rum3	brachydanio
692	30	44.1	446	2	07WD52_BORBP	07wd52	botdeiteila	765	30	44.1	614	2	05CKU6_CRYHO	05cku6	cryptospori
693	30	44.1	449	2	08W0M4_BRAJA	08w0m4	bradyrhizob	766	30	44.1	614	2	04KMC7_BRARE	04kmc7	brachydanio
694	30	44.1	450	2	082MF2_STRAW	082mf2	streptomyces	767	30	44.1	616	2	07SHN7_NEUCR	07shn7	neuospora
695	30	44.1	452	2	082S97_NITEU	082s97	nitelostoma	768	30	44.1	619	2	05EMU0_MAGGR	05emu0	magnaporthe
696	30	44.1	454	2	08YOF1_RALSO	08yof1	ralstonia s	769	30	44.1	619	2	05Z2Y4_MAGGR	05z2y4	magnaporthe
697	30	44.1	455	2	08FHC9_ECOL6	08fhc9	escherichia	770	30	44.1	624	2	04P4J2_USTMA	04p4j2	ustilago ma
698	30	44.1	457	2	07VUM3_BORPE	07vum3	botdeiteila	771	30	44.1	624	2	08QTB3_WSSV	08qtb3	white spot
699	30	44.1	457	2	07W1Z2_BORBP	07w1z2	botdeiteila	772	30	44.1	624	2	08VB83_WSSV	08vb83	white spot
700	30	44.1	457	2	07W0X0_BORBP	07w0x0	botdeiteila	773	30	44.1	627	2	0911H4_WSSV	0911h4	white spot
701	30	44.1	458	2	07UR88_RHOBA	07ur88	rhodopirella	774	30	44.1	627	2	05BDJ7_EMENTI	05bdj7	aspergillus
702	30	44.1	459	2	05PHM3_SALPA	05phm3	salmonella	775	30	44.1	627	2	07UKV6_RHOBA	07ukv6	rhodopirella
703	30	44.1	459	2	08Z6Z5_SALTT	08z6z5	salmonella	776	30	44.1	630	2	05SKU7_CRYNE	05sku7	cryptococcu
704	30	44.1	459	2	08JDE6_COXBU	08jde6	coxsiella bu	777	30	44.1	630	2	04WC67_ASPFU	04wc67	aspergillus
705	30	44.1	463	2	04NHJ2_9MICC	04nhj2	arthrobacte	778	30	44.1	630	2	0410B7_GIBZE	0410b7	gibberella
706	30	44.1	463	2	06J6R1_BACCZ	06j6r1	bacillus ce	779	30	44.1	630	2	074EH3_GEOSL	074eh3	geobacter s
707	30	44.1	465	2	065XC9_ORYSA	065xc9	oryza sativ	780	30	44.1	635	2	05KAX4_CRYNE	05kax4	cryptococcu
708	30	44.1	467	2	04LYN1_9BURK	04lyn1	burkholderi	781	30	44.1	645	2	08UHN7_AGRTS	08uhn7	agrobacteri
709	30	44.1	469	2	09HYJ1_PSEBE	09hyj1	pseudomonas	782	30	44.1	646	2	04RTU9_9SPHN	04rtu9	erythrobact
710	30	44.1	471	2	097U43_SULSO	097u43	sulfolobus	783	30	44.1	672	2	07D1J4_AGRTS	07d1j4	agrobacteri
711	30	44.1	479	2	074I52_IACCO	074i52	lactobacill	784	30	44.1	683	1	EFGL_TREDB	efgl	treponema d
712	30	44.1	493	2	04JAC9_SULAC	04jac9	sulfolobus	785	30	44.1	683	1	EFGL_TREPA	efgl	treponema p
713	30	44.1	495	2	06ZTF2_CABBR	06ztf2	caenorhabdi	786	30	44.1	690	1	ERG_ANAMM	erg	anamni
714	30	44.1	495	2	06N0U9_RHOPA	06n0u9	rhodopseudo	787	30	44.1	691	1	ERG_WOLPH	erg	wolbachia p
715	30	44.1	495	2	092U03_RHIME	092u03	rhizobium m	788	30	44.1	691	1	04W5Y1_DESVU	04w5y1	desulfovibr
716	30	44.1	503	2	057PDI_SALCH	057pdi	salmonella	789	30	44.1	691	2	06NLIC_ARATH	06nlc1	arabidopsi
717	30	44.1	508	2	07NMJ4_GLOVI	07nmj4	gloeobacter	790	30	44.1	706	2	04P505_USTMA	04p505	ustilago ma
718	30	44.1	509	2	084LIO_HORVD	084lio	hordeum vul	791	30	44.1	712	2	06NUT5_BRARE	06nut5	brachydanio
719	30	44.1	514	2	09SLJ9_ARATH	09slj9	arabidopsi	792	30	44.1	784	2	04SRA2_TESTNG	04sra2	tetradion n
720	30	44.1	517	1	FOXN4_HUMAN	096fz1	homo sapien	793	30	44.1	804	2	04ILZ0_9BURK	04ilz0	burkholderi
721	30	44.1	517	1	089XU0_BRAJA	089xj0	bradyrhizob	794	30	44.1	804	2	09HUN7_PSEAE	09hun7	pseudomonas
722	30	44.1	521	2	000908_9FUNG	000908	glomus vers	795	30	44.1	830	2	09HUN7_PSEAE	09hun7	pseudomonas
723	30	44.1	521	2	08H6E0_HORVD	08h6e0	hordeum vul	796	30	44.1	866	1	NASA_KLEBX	06k657	klebsiella
724	30	44.1	525	2	07YMD9_WHEAT	07ymd9	tritium ae	797	30	44.1	872	2	06K6A1_ORYSA	06k6a1	oryza sativ
725	30	44.1	525	2	084LH9_HORVD	084lh9	hordeum vul	798	30	44.1	894	2	05IDB8_ENTHI	05idb8	entamoeba h
726	30	44.1	525	2	084TL8_HORVU	084tl8	hordeum vul	799	30	44.1	897	1	YF67_CAEEL	yf67	caenorhabdi
727	30	44.1	525	2	093WQ8_9POL	093wq8	tritium ae	800	30	44.1	897	2	06PGT6_BRARE	06pgt6	brachydanio
728	30	44.1	525	2	093WQ9_9POL	093wq9	tritium ae	801	30	44.1	957	2	0511Q7_ENTHI	0511q7	entamoeba h
729	30	44.1	525	2	093WRO_9POL	093wro	tritium ae	802	30	44.1	994	2	09LYC8_MOUSE	09lyc8	mus musculu
730	30	44.1	526	2	07XDZ7_ORYSA	07xdz7	oryza sativ	803	30	44.1	1093	2	09BHM9_9MICR	09bhm9	pleistophor
731	30	44.1	526	2	08H6H3_ORYSA	08h6h3	oryza sativ	804	30	44.1	1106	2	08A340_BACTN	08a340	bacteroides
732	30	44.1	527	2	05GUM2_ORYSA	05gum2	oryza sativ	805	30	44.1	1117	2	09BHM2_9MICR	09bhm2	pleistophor
733	30	44.1	527	2	08H6H4_ORYSA	08h6h4	oryza sativ	806	30	44.1	1140	1	DBB1_CERAE	dbb1	cercopithec
734	30	44.1	528	2	05G0U1_ORYSA	05g0u1	oryza sativ	807	30	44.1	1140	1	DBB1_HUMAN	dbb1	homo sapien
735	30	44.1	534	2	08GSD9_ORYSA	08gsd9	oryza sativ	808	30	44.1	1140	2	05R649_PONPY	05r649	pongo pygma
736	30	44.1	534	2	09EWX5_STRCO	09ewx5	streptomyces	809	30	44.1	1140	2	09ESMO_RAT	09esmo	rattus norv
737	30	44.1	535	2	0828X0_STRAW	0828x0	ustilago ma	810	30	44.1	1140	2	09GYKO_MOUSE	09gyko	mus musculu
738	30	44.1	539	2	04PDE5_USTMA	04pdes	ustilago ma	811	30	44.1	1140	2	09WUJ9_MOUSE	09wu9	mus musculu
739	30	44.1	539	2	06GUR9_MAIZE	06gur9	zea mays (m	812	30	44.1	1140	2	0805F9_CHICK	0805f9	gallus gall
740	30	44.1	539	2	08HRS2_PSEPK	08hrs2	pseudomonas	813	30	44.1	1140	2	06P6Z0_XENLA	06p6z0	xenopus lae
741	30	44.1	541	2	08H074_ORYSA	08h074	oryza sativ	814	30	44.1	1140	2	096740_DROME	096740	drosophila
742	30	44.1	541	2	08H6G5_ORYSA	08h6g5	oryza sativ	815	30	44.1	1150	2	091R21_9VIRU	091r21	regina rana
743	30	44.1	545	2	08H6G8_ORYSA	08h6g8	oryza sativ	816	30	44.1	1165	2	06YH54_9VIRU	06yh54	amblyoma t
744	30	44.1	545	2	061FBI_CABBR	061fbi	caenorhabdi	817	30	44.1	1322	2	06UDM4_PLAFA	06udm4	pleasmodium
745	30	44.1	550	2	09DGJ0_BRARE	09dgj0	brachydanio	818	30	44.1	1322	2	XDH_RAT	xdh	rattus norv
746	30	44.1	550	2	09PT94_BRARE	09pt94	brachydanio	819	30	44.1	1330	1	XDH_MOUSE	xdh	mus musculu
747	30	44.1	556	2	09GU92_9TRYP	09gu92	trypanosoma	820	30	44.1	1337	2	04P938_USTMA	04p938	ustilago ma
748	30	44.1	556	2	09VFG2_DROME	09vfg2	drosophila	821	30	44.1	1450	2	057TT4_9TRYP	057tt4	trypanosoma
749	30	44.1	557	2	08MTJ1_DROME	08mtj1	drosophila	822	30	44.1	1450	2	04SKY6_TESTNG	04sky6	tetradion n
750	30	44.1	557	2	09VFG1_DROME	09vfg1	drosophila	823	30	44.1	1615	2	09Y061_CAEEL	09y061	caenorhabdi
751	30	44.1	558	2	08KLT0_RHISH	08klt0	rhizobium s	824	30	44.1	2514	2	0222S8_CAEEL	0222s8	caenorhabdi
752	30	44.1	560	2	04IM24_GIBZE	04im24	gibberella	825	30	44.1	2531	2	062B79_BURMA	062b79	burkholderi
753	30	44.1	560	2	09VFG0_DROME	09vfg0	drosophila	826	30	44.1	2839	2	05N1B8_BURPS	05n1b8	burkholderi
754	30	44.1	565	2	04V514_DROME	04v514	drosophila	827	30	44.1	2842	2	041892_9FLAV	041892	hepaticid g
755	30	44.1	566	2	09WZU1_THEMA	09wzu1	thermocoga	828	30	44.1	2967	2	06R5V1_MEHVI	06r5v1	meleagrid h
756	30	44.1	572	2	091TK6_TTHYV	091tk6	tupaiid ner	829	30	44.1	3325	2	091B75_MEHVI	091b75	meleagrid h
757	30	44.1	575	2	09BKR9_CAEEL	09bkr9	caenorhabdi	830	30	44.1	3342	2	091B75_MEHVI	091b75	meleagrid h
758	30	44.1	575	2	06KXG0_XENLA	06kxg0	xenopus lae	831	30	44.1	3342	2	0956N3_MEHVI	0956n3	meleagrid h
759	30	44.1	578	2	08DCK1_VIBVU	08dck1	vibrio vuln	832	30	44.1	82	2	04STZ7_TESTNG	04stz7	tetradion n
760	30	44.1	578	2	07MHA6_VIBVY	07mha6	vibrio vuln	833	30	44.1	180	2	09SGH5_ARATH	09sgh5	arabidopsi
761	30	44.1	585	2	04V539_DROME	04v539	drosophila	834	29.5	43.4	319	2	06P298_BRARE	06p298	brachydanio

835	29.5	43.4	321	2	Q561P6	BRABE	0561P6	brachydanio	908	29	42.6	336	2	Q4J4G0	AZOV1	04J4G0	azotobacter
836	29.5	43.4	917	2	Q89KU0	BRABA	089KU0	bradyrhizob	909	29	42.6	338	2	Q89RL0	STRCO	089RL0	streptomyces
837	29.5	43.4	1000	2	Q8JUM3	9NICT	08JUM3	mamestra co	910	29	42.6	343	2	Q82RC2	STTAM	082RC2	strepitomyces
838	29.5	43.4	1064	2	Q57V44	9TFRP	057V44	trypanosoma	911	29	42.6	344	2	Q87D70	XYLFT	087D70	xylophila faa
839	29	42.6	77	2	Q96481	PLABE	096481	plasmidium	912	29	42.6	344	2	Q9PB22	XYLEA	09PB22	xylophila faa
840	29	42.6	78	2	Q4YA70	PLABE	04YA70	plasmidium	913	29	42.6	349	2	Q9RW33	DEIRA	09RW33	deinococcus
841	29	42.6	84	2	Q7YRW7	CAPHI	07YRW7	capra hircu	914	29	42.6	352	2	Q50170	MYCLE	050170	mycobacteri
842	29	42.6	96	2	Q95J81	HORSE	095J81	equus caball	915	29	42.6	354	2	Q6LH52	PHOPR	06LH52	photobacter
843	29	42.6	98	2	Q9YR19	HCV	09YR19	human cytom	916	29	42.6	356	2	Q9NFP0	LEIMA	09NFP0	leishmania
844	29	42.6	100	2	Q9YR19	HCV	09YR19	human cytom	917	29	42.6	357	2	Q22066	CABEL	022066	caenorhabdit
845	29	42.6	106	2	Q7VXJ2	BORBE	07VXJ2	bordelella	918	29	42.6	358	2	Q57588	FUGRU	057588	fugu rubrip
846	29	42.6	106	2	Q7W8X7	BORBA	07W8X7	bordelella	919	29	42.6	361	2	Q96M90	HUMAN	096M90	human sapien
847	29	42.6	106	2	Q7W8X8	BORBA	07W8X8	bordelella	920	29	42.6	362	2	Q7UITS	MYCBO	07UITS	mycobacteri
848	29	42.6	110	2	Q8VJMS	MYCTU	08VJMS	mycobacteri	921	29	42.6	362	2	Q06408	MYCTU	006408	mycobacteri
849	29	42.6	111	2	Q8ZWI2	PYABE	08ZWI2	pyrobaculum	922	29	42.6	368	2	Q72R11	LEPIC	072R11	leptospira
850	29	42.6	113	2	Q4U078	AZOV1	04U078	azotobacter	923	29	42.6	368	2	Q8F489	LEPIN	08F489	leptospira
851	29	42.6	115	2	Q8P2H1	METMA	08P2H1	methanosarc	924	29	42.6	368	2	Q9CBB8	MYCLE	09CBB8	mycobacteri
852	29	42.6	115	2	Q95802	DROME	095802	drosophila	925	29	42.6	371	2	Q97205	SULSO	097205	sulfolobus
853	29	42.6	127	2	Q76992	TAEBA	076992	taenia sagi	926	29	42.6	371	2	Q61KY7	CABBR	061KY7	caenorhabdit
854	29	42.6	127	2	Q8RMJ4	CAMJE	08RMJ4	campylobact	927	29	42.6	372	2	Q4JBP2	SUTAC	04JBP2	sulfolobus
855	29	42.6	127	2	Q5HSN5	CAMJR	05HSN5	campylobact	928	29	42.6	374	2	Q974L5	SUITO	0974L5	sulfolobus
856	29	42.6	130	1	OSTN	MOUSE	OSTN	mus musculu	929	29	42.6	377	2	Q8PYZ6	METMA	08PYZ6	methanosarc
857	29	42.6	132	1	OSTN	RAT	OSTN	rattus norv	930	29	42.6	385	2	Q9NFP1	LEIMA	09NFP1	leishmania
858	29	42.6	133	1	OSTN	HUMAN	OSTN	homo sapien	931	29	42.6	386	2	Q8RY43	SECCO	08RY43	secale cere
859	29	42.6	137	2	Q97D00	CLOAB	097D00	clostridium	932	29	42.6	387	2	Q5C092	CRYPV	05C092	cryptospori
860	29	42.6	145	2	Q4N7A8	THEBA	04N7A8	theileria p	933	29	42.6	392	2	Q6NNM8	DROME	06NNM8	drosophila
861	29	42.6	145	2	Q9JX84	NEIMA	09JX84	neisseria m	934	29	42.6	392	2	Q4YD11	9POLA	04YD11	9polus trile
862	29	42.6	145	2	Q9K1B7	NEIMB	09K1B7	neisseria m	935	29	42.6	392	2	Q4YD11	9POLA	04YD11	9polus trile
863	29	42.6	150	2	Q6ZV54	HUMAN	06ZV54	homo sapien	936	29	42.6	396	2	Q6LPO0	PHOPR	06LPO0	photobacter
864	29	42.6	150	2	Q7MUJ8	PORGI	07MUJ8	porphyromon	937	29	42.6	398	2	Q5KYE5	GEOKA	05KYE5	geobacillus
865	29	42.6	152	2	Q8MPC5	TAEBO	08MPC5	taenia soli	938	29	42.6	399	1	PHHC	PSBAE	PHHC	psaerobact
866	29	42.6	161	2	Q8NARI	HUMAN	08NARI	homo sapien	939	29	42.6	399	2	Q21342	CABEL	021342	caenorhabdit
867	29	42.6	166	2	Q4YUAG	PLACH	04YUAG	plasmidium	940	29	42.6	403	2	Q746S0	GEBEL	0746S0	geobacter s
868	29	42.6	169	2	Q9PVQ0	XENLA	09PVQ0	xenopus lae	941	29	42.6	404	2	Q5Y953	HUMAN	05Y953	human sapien
869	29	42.6	170	2	Q4YSV7	PLABE	04YSV7	plasmidium	942	29	42.6	406	2	Q9J955	MOUSE	09J955	mus musculu
870	29	42.6	173	2	Q8FRJ6	COREF	08FRJ6	corynebacte	943	29	42.6	408	2	Q7D717	MYCTU	07D717	mycobacteri
871	29	42.6	191	2	Q7NV46	CHROV	07NV46	chryseobacte	944	29	42.6	409	2	Q5B2N7	EMENI	05B2N7	emmental
872	29	42.6	192	2	Q00503	9HYPO	000503	calonectria	945	29	42.6	409	2	Q5HQD4	SILPO	05HQD4	silicibacte
873	29	42.6	192	2	Q4TLB8	9SPHN	04TLB8	erythrobact	946	29	42.6	409	2	Q5PQPO	RAT	05PQPO	rattus norv
874	29	42.6	211	2	Q4Z083	PLABE	04Z083	plasmidium	947	29	42.6	414	2	Q9RMV4	VIBCH	09RMV4	vibriochol
875	29	42.6	215	1	DEOC	LACPL	DEOC	lactobacilli	948	29	42.6	419	1	GLPB	ECOL6	GLPB	escherichia
876	29	42.6	215	1	Q67M34	SYMTH	067M34	syntrophomon	949	29	42.6	419	1	GLPB	ECOL6	GLPB	escherichia
877	29	42.6	216	2	Q5LRCA	SILPO	05LRCA	silicibacte	950	29	42.6	419	1	GLPB	ECOL6	GLPB	escherichia
878	29	42.6	217	2	Q01730	BRALA	001730	brachyobact	951	29	42.6	419	1	GLPB	ECOL6	GLPB	escherichia
879	29	42.6	224	2	Q98NM0	RHILLO	098NM0	rhizobium l	952	29	42.6	422	2	Q8ZUIS	PIYAB	08ZUIS	pyrobaculum
880	29	42.6	224	2	Q6TUF5	RAT	06TUF5	rattus norv	953	29	42.6	422	2	Q5QM70	ORSA	05QM70	oryza sativ
881	29	42.6	236	2	Q6ETZ8	ORSA	06ETZ8	oryza sativ	954	29	42.6	422	2	Q7TZB7	MYCBO	07TZB7	mycobacteri
882	29	42.6	237	2	Q5SUX9	MOUSE	05SUX9	mus musculu	955	29	42.6	424	2	Q07730	MYCTU	007730	mycobacteri
883	29	42.6	237	2	Q89M29	BRABA	089M29	bradyrhizob	956	29	42.6	424	2	Q55F21	DICDI	055F21	dicyclosteli
884	29	42.6	243	2	Q75BA1	ASHGO	075BA1	ashbya goss	957	29	42.6	426	2	Q4UVU6	XANCP	04UVU6	xanthomonas
885	29	42.6	244	2	Q851B5	ORYSA	0851B5	oryza sativ	958	29	42.6	426	2	Q8PB91	XANCP	08PB91	xanthomonas
886	29	42.6	252	2	Q6FCJ5	ACTIAD	06FCJ5	actinobact	959	29	42.6	428	2	Q5NBT1	PRATT	05NBT1	pratt
887	29	42.6	263	2	Q98KE1	RHILLO	098KE1	rhizobium l	960	29	42.6	428	2	Q5WXC7	LEBPL	05WXC7	leishmania
888	29	42.6	264	2	Q8AM09	BRABE	08AM09	brachydanio	961	29	42.6	429	1	SYA	CORGL	SYA	corynebacte
889	29	42.6	265	2	Q915Y6	PSBAE	0915Y6	pseudomonas	962	29	42.6	430	2	Q4NLY3	9MTCO	04NLY3	methanobact
890	29	42.6	275	2	Q6D6X8	BRMCT	06D6X8	erythrobact	963	29	42.6	431	2	Q54041	PSBAE	054041	pseudomonas
891	29	42.6	280	2	Q85U22	ENCCU	085U22	encephalito	964	29	42.6	431	2	Q8CC26	MOUSE	08CC26	mus musculu
892	29	42.6	280	2	Q5PI53	AZOSE	05PI53	azocarcus sp	965	29	42.6	432	2	Q5JXMI	HUMAN	05JXMI	human sapien
893	29	42.6	280	2	Q5LYZ3	NOCFA	05LYZ3	nocardia fa	966	29	42.6	434	2	Q4LRB1	9BURK	04LRB1	burkholderi
894	29	42.6	281	2	Q6M140	METMP	06M140	methanococc	967	29	42.6	434	2	Q63T22	BURPS	063T22	burkholderi
895	29	42.6	283	2	Q53R38	HUMAN	053R38	homo sapien	968	29	42.6	434	2	Q8UDN2	AGRTS	08UDN2	agrobacteri
896	29	42.6	286	2	Q7Z743	BRABE	07Z743	brachydanio	969	29	42.6	434	2	Q7TMUB	MOUSE	07TMUB	mus musculu
897	29	42.6	290	2	Q874S9	AEDAB	0874S9	aedes aegypt	970	29	42.6	435	2	Q553Q5	DICDI	0553Q5	dicyclosteli
898	29	42.6	290	2	Q874T0	AEDAB	0874T0	aedes aegypt	971	29	42.6	435	2	Q6G2S7	BARBE	06G2S7	bartonella
899	29	42.6	290	2	Q874T1	AEDAB	0874T1	aedes aegypt	972	29	42.6	435	2	Q6N7B6	RHOPA	06N7B6	rhodopseud
900	29	42.6	290	2	Q874T2	AEDAB	0874T2	aedes aegypt	973	29	42.6	437	2	Q891V5	BRABA	0891V5	bradyrhizob
901	29	42.6	290	2	Q95P61	AEDAB	095P61	aedes aegypt	974	29	42.6	438	1	SHIA	ECOLI	SHIA	escherichia
902	29	42.6	290	2	Q9BUMB	AEDAB	09BUMB	aedes aegypt	975	29	42.6	438	1	Q8RR46	ESCFE	08RR46	escherichia
903	29	42.6	290	2	Q5A4U4	CANAL	05A4U4	canal alb	976	29	42.6	438	2	Q7ACT1	ECOS7	07ACT1	escherichia
904	29	42.6	295	2	Q810T0	CANAL	0810T0	mus musculu	977	29	42.6	438	2	Q65UQ7	MANSM	065UQ7	mannheimia
905	29	42.6	314	2	Q7UPUS	RHOBA	07UPUS	rhodospirell	978	29	42.6	438	2	Q8X4U5	ECOS7	08X4U5	escherichia
906	29	42.6	315	2	Q75CB3	ASHGO	075CB3	ashbya goss	979	29	42.6	438	2	Q8RGD5	ECOL6	08RGD5	escherichia
907	29	42.6	329	2					980	29	42.6	438	2				

```

981 29 42.6 440 1 YH4E_ECOLI P37643 escherichia
982 29 42.6 440 2 O57Y13_SALCH O57113 salmonella
983 29 42.6 440 2 O5PUP3_SALPA O5P1P5 salmonella
984 29 42.6 440 2 O8JPS5_SHIFL O8JPS5 shigella fl
985 29 42.6 440 2 O8FC10_ECOL6 O8FC10 escherichia
986 29 42.6 440 2 O8X4K9_ECO57 O8X4K9 escherichia
987 29 42.6 440 2 O8Z282_SALTI O8Z282 salmonella
988 29 42.6 440 2 O8ZIC3_SALTY O8ZIC3 salmonella
989 29 42.6 441 2 O6D950_ERMCT O6D950 erwina car
990 29 42.6 442 2 O8PUP6_XANAC O8PUP6 xanthomonas
991 29 42.6 443 2 O4JVE8_CORJK O4JVE8 corynebacte
992 29 42.6 443 2 O6ZIU8_BURMA O6ZIU8 burkholderi
993 29 42.6 445 2 O8BK80_PSEBK O8BK80 pseudomonas
994 29 42.6 446 2 O4RFP0_TERNG O4RFP0 tetracodon n
995 29 42.6 447 2 O635U3_BURSK O635U3 burkholderi
996 29 42.6 448 2 O931D3_PSEYM O931D3 pseudomonas
997 29 42.6 448 2 O88BNI_PSESM O88BNI pseudomonas
998 29 42.6 448 2 O88BT7_PSESM O88BT7 pseudomonas
999 29 42.6 449 2 O45082_BURCE O45082 burkholderi
1000 29 42.6 451 1 MURD_GEOXA O510X7 geobacillus

```

ALIGNMENTS

```

RESULT 1
ID 06VYM3_BRARE PRELIMINARY; PRT; 106 AA.
AC 06VYM3;

```

```

DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DE 05-JUL-2004 (Tremblrel. 27, Last annotation update)

```

```

DE Atrial natriuretic factor.

```

```

GN Name=nppa;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxId=7955;

```

```

RN NCB1_TaxId=7955;

```

```

RX NUCLEOTIDE SEQUENCE.

```

```

RA MEDLINE=22959386; PubMed=14573521; DOI=10.1242/dev.00838;
RA Berdugo E., Coleman H., Lee D.H., Stainier D.Y., Yelon D.;
"Mutation of weak atrium/atrial myosin heavy chain disrupts atrial
function and influences ventricular morphogenesis in zebrafish.";
RT Development 130:6121-6129(2003).

```

```

RL EMBL; AY319419; AAQ87026.1; -; mRNA.

```

```

DR ZFIN; ZDB-GENE-030131-95; nppa.

```

```

DR GO; GO:0005576; C:extracellular region; IEA.

```

```

DR GO; GO:0005179; F:hormone activity; IEA.

```

```

DR GO; GO:0050880; P:regulation of blood vessel size; IEA.

```

```

DR InterPro; IPR000663; Natri_peptide.

```

```

DR Pfam; PF00212; ANP; 1.

```

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DR PRINTS; PR00710; NATPEPTIDES.

```

```

DR ProDom; PD005617; Natri_peptide; 1.

```

```

DR SMART; SM00183; NAT_PEP; 1.

```

```

DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.

```

```

DR VASOACTIVE.

```

```

SQ SEQUENCE 106 AA; 11528 MW; C44A659CD9DFE9CA CRC64;

```

```

Query Match 83.8%; Score 57; DB 2; Length 106;
Best Local Similarity 58.8%; Pred. NO. 0.00027;

```

```

Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

```

QY 1 CFGXXXXRIGXXSXGC 17
||| ||| ||| |||
DB 85 CFGGRIDRIGSSSTLGC 101

```

```

RESULT 2
ANF_ACITR STANDARD; PRT; 142 AA.
AC P83564;

```

```

DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Atrial natriuretic factor precursor (ANF) (Atrial natriuretic peptide)
DE (ANP) (Prepronatriodilatin).
GN Name=NP;
OS Acipenser transmontanus (White sturgeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae;
OC Acipenser.
NCBI_TaxId=7904;

```

```

[1]

```

```

RP NUCLEOTIDE SEQUENCE, AND TISSUE SPECIFICITY.

```

```

RC PubMed=15072558; DOI=10.1677/jme.0.0320547;

```

```

RX Kawakoshi A., Hyodo S., Inoue K., Kobayashi Y., Takei Y.;

```

```

RA "Four natriuretic peptides (ANP, BNP, VNP and CNP) coexist in the

```

```

RT sturgeon: identification of BNP in fish lineage.";

```

```

RL J. Mol. Endocrinol. 32:547-555(2004).

```

```

CC -!- FUNCTION: A potent vasoactive substance which is thought to play a

```

```

CC key role in cardiovascular homeostasis. Has a GMP-stimulating

```

```

CC activity.

```

```

CC -!- SUBCELLULAR LOCATION: Secreted.

```

```

CC -!- TISSUE SPECIFICITY: Expressed in heart atrium and to a lower

```

```

CC extent in heart ventricle, but not in brain.

```

```

CC -!- SIMILARITY: Belongs to the natriuretic peptide family.

```

```

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

```

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CC -----

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```

DR EMBL; AB087728; BAD02835.1; -; mRNA.

```

```

DR InterPro; IPR002407; At_natriurtcep.

```

```

DR InterPro; IPR002408; Br_natriurtcep.

```

```

DR InterPro; IPR000663; Natri_peptide.

```

```

DR PANTHER; PTHR11415; At_natriurtcep; 1.

```

```

DR Pfam; PF00212; ANP; 1.

```

```

DR PRINTS; PR00712; BNATPEPTIDE.

```

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DR PRINTS; PR00710; NATPEPTIDES.

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DR ProDom; PD005617; Natri_peptide; 1.

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DR SMART; SM00183; NAT_PEP; 1.

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DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.

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KM Hormone; Signal; Vasoactive.

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FT SIGNAL 1 23 Potential.

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FT PROPEP 24 111 Atrial natriuretic factor.

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FT PEPTIDE 113 142 By similarity.

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FT DISULFID 120 136

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SQ SEQUENCE 142 AA; 15888 MW; 382B87FB44178CD9 CRC64;

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Query Match 83.8%; Score 57; DB 1; Length 142;
Best Local Similarity 58.8%; Pred. NO. 0.00035;

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Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 1 CFGXXXXRIGXXSXGC 17
||| ||| ||| |||
DB 120 CFGSRIDRIGSSWMC 136

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RESULT 3
Q7T217_ONCMY PRT; 146 AA.

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ID Q7T217_ONCMY PRELIMINARY;
AC Q7T217;

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DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)

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DE 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Atrial natriuretic peptide.

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GN Name=anp;

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OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

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OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

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OX NCBI_TaxId=8022;
 RN [1]
 RA NUCLEOTIDE SEQUENCE.
 RP Inoue K., Russel M.J., Olson K.R., Takei Y.,
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB076603; BAC77769.1; -; mRNA.
 DR GO: GO:0005576; C:extracellular region; IEA.
 DR GO: GO:0005179; F:hormone activity; IEA.
 DR GO: GO:0007582; P:physiological process; IEA.
 DR GO: GO:0050880; P:regulation of blood vessel size; IEA.
 DR InterPro: IPR002407; At_natriureticp.
 DR Pfam: PF00212; ANP; 1.
 DR PRINTS: PR00711; ANATPEPTIDE.
 DR PRODOM: PD005617; Natr_peptide; 1.
 DR SMART: SM00183; NAT_PEP; 1.
 DR PROSITE: PS00263; NATRIURETIC_PEPIDE; 1.
 KW Vasoactive.
 SQ SEQUENCE 146 AA; 16043 MW; FEDCE3C79121BD0 CRC64;

Query Match 83.8%; Score 57; DB 2; Length 146;
 Best Local Similarity 58.8%; Pred. No. 0.00036;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXXRIGXXSXXGC 17
 DB 124 CFGAMMDRIGTSSGLGC 140

RESULT 4

O78AW6_SALSA PRELIMINARY; PRT; 148 AA.
 AC O78AW6;
 DT 05-JUL-2004 (TRENBLREL. 27, Created)
 DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
 DE Cardiac peptide precursor.
 OS Salmo salar (Atlantic salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 OX NCBI_TaxId=8030;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20114377; PubMed=10650955; DOI=10.1210/en.141.2.731;
 RA Majalahti-Palviainen T., Hirvonen M., Tervonen V., Ilves M.,
 RA Ruskosaho H., Vuolteenaho O.;
 RT "Gene structure of a new cardiac peptide hormone: a model for heart-
 specific gene expression.";
 RL Endocrinology 141:731-740(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Vuolteenaho O.J.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ006421; CA07023.1; -; Genomic DNA.
 DR GO: GO:0005576; C:extracellular region; IEA.
 DR GO: GO:0005179; F:hormone activity; IEA.
 DR GO: GO:0007582; P:physiological process; IEA.
 DR GO: GO:0050880; P:regulation of blood vessel size; IEA.
 DR InterPro: IPR002407; At_natriureticp.
 DR Pfam: PF00212; ANP; 1.
 DR PRINTS: PR00711; ANATPEPTIDE.
 DR PRODOM: PD005617; Natr_peptide; 1.
 DR SMART: SM00183; NAT_PEP; 1.
 DR PROSITE: PS00263; NATRIURETIC_PEPIDE; 1.
 KW Signal; Vasoactive.
 FT SIGNAL 1 119 Potential.
 FT CHAIN 120 148 cardiac peptide.
 SQ SEQUENCE 148 AA; 16236 MW; 934985642C25C739 CRC64;

Query Match 83.8%; Score 57; DB 2; Length 148;
 Best Local Similarity 58.8%; Pred. No. 0.00036;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXXRIGXXSXXGC 17
 DB 126 CFGAMMDRIGTSSGLGC 142

RESULT 5

O9YGJ1_SALSA PRELIMINARY; PRT; 152 AA.
 AC O9YGJ1;
 DT 01-MAY-1999 (TRENBLREL. 10, Created)
 DT 01-MAY-1999 (TRENBLREL. 10, Last sequence update)
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
 DE Cardiac hormone.
 OS Salmo salar (Atlantic salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 OX NCBI_TaxId=8030;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Tervonen V., Arjamaa O., Ruskosaho H., Vuolteenaho O.;
 RT "New vasoactive cardiac hormone released by mechanical load.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Vuolteenaho O.J.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ001806; CA05022.1; -; mRNA.
 DR GO: GO:0005576; C:extracellular region; IEA.
 DR GO: GO:0005179; F:hormone activity; IEA.
 DR GO: GO:0007582; P:physiological process; IEA.
 DR GO: GO:0050880; P:regulation of blood vessel size; IEA.
 DR InterPro: IPR002407; At_natriureticp.
 DR InterPro: IPR000663; Natr_peptide.
 DR Pfam: PF00212; ANP; 1.
 DR PRINTS: PR00711; ANATPEPTIDE.
 DR PRODOM: PD005617; Natr_peptide; 1.
 DR SMART: SM00183; NAT_PEP; 1.
 DR PROSITE: PS00263; NATRIURETIC_PEPIDE; 1.
 KW Vasoactive.
 FT CHAIN 124 152 cardiac hormone.
 SQ SEQUENCE 152 AA; 16740 MW; E1D3E38A159CFEEA CRC64;

Query Match 83.8%; Score 57; DB 2; Length 152;
 Best Local Similarity 58.8%; Pred. No. 0.00037;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXXRIGXXSXXGC 17
 DB 130 CFGAMMDRIGTSSGLGC 146

RESULT 6

ANF_RANRI STANDARD; PRT; 30 AA.
 AC P09196;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Atrial natriuretic factor (ANF) (Atrial natriuretic peptide) (ANP).
 OS Rana ridibunda (laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana;
 OC Pelophylax.
 OX NCBI_TaxId=8406;
 RN [1]
 RP PROTEIN SEQUENCE.
 RT TISSUE=Heart atrium;

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RX MEDLINE=89005705; PubMed=2971573; DOI=10.1016/0014-5793(88)80501-5;
RA Lazare C., Ong H., McNicoll N., Netchitailo P., Chretien M.,
RA de Lean A., Vaudry H.;
RT "The amino acid sequences of frog heart atrial natriuretic-like
RT peptide and mammalian ANP are closely related.";
RL FEBS Lett. 238:300-306 (1988).
CC -!- FUNCTION: A potent vasoactive substance which is thought to play a
CC key role in cardiovascular homeostasis. Has a cGMP-stimulating
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR: S01657; S01657.
DR InterPro: IPR002407; At_natriurtcep.
DR InterPro: IPR002408; Br_natriurtcep.
DR InterPro: IPR000663; Natr_peptide.
DR PANTHER: PTHR11415; At_natriurtcep; 1.
DR Pfam: PF00212; ANP; 1.
DR PRINTS: PR00712; BNATPEPTIDE.
DR PRINTS: PR00710; NATPEPTIDES.
DR ProDom: PD005107; At_natriurtcep; 1.
DR SMART: SM00183; NAT_PEP; 1.
DR PROSITE: PS00263; NATRIURETIC_PEPPTIDE; 1.
DR Direct protein sequencing; Hormone; Vasoactive.
KW DISULFID 11
FT SEQUENCE 30 AA; 3263 MW; 175A946321C27DA0 CRC64;
SQ
Query Match 82.4%; Score 56; DB 1; Length 30;
Best Local Similarity 58.8%; Pred. No. 0.00014;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 CCGXXXDRIGXXSXXGC 17
DB 11 CCGSRIDRIGASGMC 27
RESULT 7
Q4TD23_TENG 83 AA.
ID Q4TD23_TENG PRELIMINARY; PRT; 83 AA.
AC Q4TD23;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF6568, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0003028001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
[1]
RN NUCLEOTIDE SEQUENCE.
RP Jallou O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
RA Mauceli E., Bouneue L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Sallanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castell V., Katinka M., Vacherie B.,
RA Blemont C., Skali Z., Catolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brotier P., Coutanceau J.P., Guzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McSwan P., Bosak S.,
RA Kellis M., Volt J.N., Guigo R., Zody M.C., Mesitov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lauder V., Schacher V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals

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RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957 (2004).
[2]
RN NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
DR EMBL: CAAE01006568; CAA9209.1; -; Genomic_DNA.
DR InterPro: IPR002408; Br_natriurtcep.
DR InterPro: IPR000663; Natr_peptide.
DR Pfam: PF00212; ANP; 1.
DR PRINTS: PR00712; BNATPEPTIDE.
DR PRINTS: PR00710; NATPEPTIDES.
DR ProDom: PD005617; Natr_peptide; 1.
DR SMART: SM00183; NAT_PEP; 1.
DR PROSITE: PS00263; NATRIURETIC_PEPPTIDE; 1.
KW Vasoactive.
KW NON_TER 83
FT SEQUENCE 83 AA; 9432 MW; 5D02DD1512E2D6 CRC64;
SQ
Query Match 82.4%; Score 56; DB 2; Length 83;
Best Local Similarity 58.8%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 CCGXXXDRIGXXSXXGC 17
DB 65 CCGRMDRIGSWSLGC 81
RESULT 8
ID ANF_CAVPO STANDARD; PRT; 128 AA.
AC P27596;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Atrial natriuretic factor precursor (ANF) (Atrial natriuretic peptide)
DE (ANP) (Prepronatriodiatin) [contains: Cardiotatin-related peptide
DE (CDP)] (Fragment).
GN Name=NPPA;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystriognath; Caviidae; Cavia.
OX NCBI_TaxID=10141;
[1]
RN NUCLEOTIDE SEQUENCE.
RP Tissue=Heart atrium;
RC Maegert H.-J., Hanke M., Schmieding G., Teuteberg K., Schulz-Knappe P.,
RA Forssmann W.-G.;
RL Submitted (MAR-1991) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: A potent vasoactive substance which is thought to play a
CC key role in cardiovascular homeostasis. Has a cGMP-stimulating
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DEVELOPMENTAL STAGE: Adult.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL: X58562; CAA41442.1; -; mRNA.
DR PIR: S14872; S14872.
DR InterPro: IPR002407; At_natriurtcep.
DR InterPro: IPR000663; Natr_peptide.
DR PANTHER: PTHR11415; At_natriurtcep; 1.
DR Pfam: PF00212; ANP; 1.
DR PRINTS: PR00711; ANATPEPTIDE.

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DR PRINTS; PR00710; NATPEPTIDES.
 DR Prodom; PD005107; At_natriureticp; 1.
 DR Prodom; PD005617; Natr_peptide; 1.
 DR SMART; SM00183; NAT_PEP; 1.
 DR PROSITE; PS00263; NATRIURETIC_PEP; 1.
 KW Hormone; Vasocactive.
 FT PEPTIDE 1 30 Cardiolipin-related peptide.
 FT PROPEP 99 126 Atrial natriuretic factor.
 FT DISULFID 105 121 By similarity.
 FT NON_TER 1 1
 SQ SEQUENCE 128 AA; 13966 MW; EFC5004B4DDEF318 CRC64;

Query Match 82.4%; Score 56; DB 1; Length 128;
 Best Local Similarity 58.8%; Pred. No. 0.00053;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFCXXXDRIGXXSXXGC 17
 Db 105 CFCGRMDRIGASSLGC 121

RESULT 9
 ANFB_FUGRU STANDARD; PRT; 133 AA.
 AC Q805D7;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Brain natriuretic peptide precursor (B-type natriuretic peptide).
 GN Name=BNP;
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 OX NCBI_TaxId=31033;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Heart;
 RX PubMed=15072558; DOI=10.1677/jme.0.0320547;
 RA Kawakoshi A., Hyodo S., Inoue K., Kobayashi Y., Takei Y.;
 RT "Four natriuretic peptides (ANP, BNP, VNP and CNP) coexist in the
 RT sturgeon: identification of BNP in fish lineage.";
 RL J. Mol. Endocrinol. 32:547-555(2004).
 CC -!- FUNCTION: Acts as a cardiac hormone with a variety of biological
 CC actions including natriuresis, diuresis, vasorelaxation, and
 CC inhibition of renin and aldosterone secretion. It is thought to
 CC play a key role in cardiovascular homeostasis. Helps restore the
 CC body's salt and water balance. Improves heart function.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AB089934; BAC57070.1; -; mRNA.
 DR Ensemble; SINFUG0000135753; Fugu rubripes.
 DR InterPro; IPR002408; Br_natriurtcep.
 DR InterPro; IPR000663; Natr_peptide.
 DR Pfam; PF00212; ANP; 1.
 DR PRINTS; PR00712; BNATPEPTIDE.
 DR PRINTS; PR00710; NATPEPTIDES.
 DR Prodom; PD005617; Natr_peptide; 1.
 DR SMART; SM00183; NAT_PEP; 1.
 DR PROSITE; PS00263; NATRIURETIC_PEP; 1.
 KW Hormone; Signal; Vasocactive.
 FT SIGNAL 1 22 Potential.
 FT PROPEP 23 7
 FT PEPTIDE ? 133 Brain natriuretic peptide.
 FT DISULFID 108 124 By similarity.

SQ SEQUENCE 133 AA; 14746 MW; FD4541B255A33436 CRC64;

Query Match 82.4%; Score 56; DB 1; Length 133;
 Best Local Similarity 58.8%; Pred. No. 0.00054;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFCXXXDRIGXXSXXGC 17
 Db 108 CFCGRMDRIGSMSSLGC 124

RESULT 10
 ANFB_OREMO STANDARD; PRT; 138 AA.
 AC Q805E8;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Brain natriuretic peptide precursor (B-type natriuretic peptide).
 GN Name=BNP;
 OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidae;
 OC Cichlidae; African cichlids; Pseudocrenilabrine; Tilapiaini;
 OC Oreochromis.
 OX NCBI_TaxId=8127;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Heart;
 RX PubMed=15072558; DOI=10.1677/jme.0.0320547;
 RA Kawakoshi A., Hyodo S., Inoue K., Kobayashi Y., Takei Y.;
 RT "Four natriuretic peptides (ANP, BNP, VNP and CNP) coexist in the
 RT sturgeon: identification of BNP in fish lineage.";
 RL J. Mol. Endocrinol. 32:547-555(2004).
 CC -!- FUNCTION: Acts as a cardiac hormone with a variety of biological
 CC actions including natriuresis, diuresis, vasorelaxation, and
 CC inhibition of renin and aldosterone secretion. It is thought to
 CC play a key role in cardiovascular homeostasis. Helps restore the
 CC body's salt and water balance. Improves heart function.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
 CC -----
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 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AB087284; BAC55025.1; -; mRNA.
 DR InterPro; IPR002408; Br_natriurtcep.
 DR InterPro; IPR000663; Natr_peptide.
 DR Pfam; PF00212; ANP; 1.
 DR PRINTS; PR00712; BNATPEPTIDE.
 DR PRINTS; PR00710; NATPEPTIDES.
 DR Prodom; PD005617; Natr_peptide; 1.
 DR SMART; SM00183; NAT_PEP; 1.
 DR PROSITE; PS00263; NATRIURETIC_PEP; 1.
 KW Hormone; Signal; Vasocactive.
 FT SIGNAL 1 22 Potential.
 FT PROPEP 23 7
 FT PEPTIDE ? 138 Brain natriuretic peptide.
 FT DISULFID 111 127 By similarity.
 SQ SEQUENCE 138 AA; 15189 MW; 5A023AB1F4F452FA CRC64;

Query Match 82.4%; Score 56; DB 1; Length 138;
 Best Local Similarity 58.8%; Pred. No. 0.00056;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFCXXXDRIGXXSXXGC 17
 Db 111 CFCGRMDRIGSMSSLGC 127


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RESULT 11
Q47953 TETNG
ID Q47953 TETNG PRELIMINARY; PRT; 138 AA.
AC Q47953;
DT 13-SEP-2005 (TEMBLrel. 31, Created)
DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)
DE Chromosome undetermined SCAR7638, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00004914001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxId=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicard S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Caselli V., Katinka M., Vacherie B.,
RA Bismont C., Skalli Z., Cattolico L., Poulain J., De Bernardis V.,
RA Cruaud C., Duprat S., Brotier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chappe C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volt J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Landel V., Schachter V., Queller F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
[2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CAAB01007638; CAF90579.1; -!- Genomic_DNA.
DR InterPro: IPR002408; Br_natriureticp.
DR InterPro: IPR000663; Natf_peptide.
DR Pfam: PF00212; ANF; 1.
DR PRINTS; PRO0712; BNATPEPTIDE.
DR PRODOM; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
FT NON_TER 138
SQ SEQUENCE 138 AA; 15212 MW; E244D7D6F9BE3BF4 CRC64;

Query Match 82.4%; Score 56; DB 2; Length 138;
Best Local Similarity 58.8%; Pred. No. 0.00056;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXSXXGC 17
DB 117 CFGARMDRIGNASGLGC 133

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OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxId=31033;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RX PubMed=15072558; DOI=10.1677/jme.0.0320547;
RA Kawakoshi A., Hyodo S., Inoue K., Kobayashi Y., Takei Y.;
RT "Four natriuretic peptides (ANP, BNP, VNP and CNP) coexist in the
RT sturgeon: identification of BNP in fish lineage.";
RL J. Mol. Endocrinol. 32:547-555(2004).
CC -!- FUNCTION: A potent vasoactive substance which is thought to play a
CC key role in cardiovascular homeostasis. Has a cGMP-stimulating
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; AB089933; BAC57069.1; -!- mRNA.
DR InterPro: IPR002407; At_natriureticp.
DR InterPro: IPR000663; Natr_peptide.
DR PANTHER; PTHR11415; At_natriureticp; 1.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PRO0710; NATPEPTIDES.
DR PRODOM; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasoactive.
FT SIGNAL 1 21
FT PROPEP 22 112
FT PEPTIDE 115 119
FT DISULFID 118 134
SQ SEQUENCE 139 AA; 15569 MW; EC9BCBE9D5C31220 CRC64;

Query Match 82.4%; Score 56; DB 1; Length 139;
Best Local Similarity 58.8%; Pred. No. 0.00057;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXSXXGC 17
DB 118 CFGARMDRIGNASGLGC 134

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RESULT 13
ANF OREMO
ID -ANF OREMO STANDARD; PRT; 140 AA.
AC Q80569;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Atrial natriuretic factor precursor (ANF) (Atrial natriuretic peptide)
DE (ANP) (Prepronatriureticin).
GN Name=ANP;
OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
OC Cichlidae; African cichlids; Pseudocrenilabrinae; Tilapini;
OC Oreochromis.
OX NCBI_TaxId=8127;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RX PubMed=15072558; DOI=10.1677/jme.0.0320547;
RA Kawakoshi A., Hyodo S., Inoue K., Kobayashi Y., Takei Y.;

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RT "Four natriuretic peptides (ANP, BNP, VNP and CNP) coexist in the
RT sturgeon: identification of BNP in fish lineage.";
RL J. Mol. Endocrinol. 32:547-555(2004).
CC -1- FUNCTION: A potent vasoactive substance which is thought to play a
CC key role in cardiovascular homeostasis. Has a cGMP-stimulating
CC activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL, AB087283; BAC55024.1; -; mRNA.
DR InterPro; IPR002407; At_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR PANTHER; PTHR11415; At_natriurtcep; 1.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
DR Hormone; Signal; Vasoactive.
KW SIGNAL.
FT PROPEP 1 21 Potential.
FT PEPTIDE 116 140 Atrial natriuretic factor.
FT DISULFID 119 135 By similarity.
SQ SEQUENCE 140 AA; 15577 MW; 5F2D214FA560DB0F CRC64;

Query Match
Best Local Similarity 82.4%; Score 56; DB 1; Length 140;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXXGC 17
DB 119 CFGAMDRIGNAGSGLGC 135

RESULT 14
ID ANF_RANCA STANDARD; PRT; 145 AA.
AC P16509;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Atrial natriuretic factor precursor (ANF) (Atrial natriuretic peptide)
DE (ANP).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Agnatha; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana;
OC Aquarana.
OX NCBI_TaxID=8400;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kojima M.;
RL Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP PROTEIN SEQUENCE OF 122-145.
RC TISSUE=Heart;
RX MEDLINE=89025806; PubMed=2972279;
RA Sakata J., Kangawa K., Matsuo H.;
RL "Identification of new atrial natriuretic peptides in frog heart.";
RT Biochem. Biophys. Res. Commun. 155:1338-1345(1988).
CC -1- FUNCTION: A potent vasoactive substance which is thought to play a
CC key role in cardiovascular homeostasis. Has a cGMP-stimulating
CC activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration

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CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL, D01043; BAA00850.1; -; mRNA.
DR PIR; J00947; J00947.
DR InterPro; IPR002407; At_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR PANTHER; PTHR11415; At_natriurtcep; 1.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00711; ANATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005107; At_natriurtcep; 1.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
DR Direct protein sequencing; Hormone; Signal; Vasoactive.
FT SIGNAL 1 23 Potential.
FT PROPEP 24 119 Atrial natriuretic factor.
FT PEPTIDE 122 145
FT DISULFID 125 141
SQ SEQUENCE 145 AA; 15934 MW; 01EB3B9779529405 CRC64;

Query Match
Best Local Similarity 82.4%; Score 56; DB 1; Length 145;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXXGC 17
DB 125 CFGSRIDRIGAGSGMGC 141

RESULT 15
ID Q5XPR8_RANRI PRELIMINARY; PRT; 145 AA.
AC Q5XPR8;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Atrial natriuretic factor.
DE Atrial natriuretic factor.
OS Rana ridibunda (laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Agnatha; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana;
OC Pelophylax.
OX NCBI_TaxID=8406;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Vasileopoulos A., Galanaki C., Papazafiri P., Beis I.;
RL "Expression of atrial natriuretic factor (ANF) in Rana ridibunda
RL pertused heart, during oxidative and mechanical stress.";
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY743415; AAU93955.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007582; P:physiological process; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002407; At_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00711; ANATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005107; At_natriurtcep; 1.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
FT CHAIN 116 145 atrial natriuretic factor.
SQ SEQUENCE 145 AA; 15909 MW; 236F242F12B74A3E CRC64;

Query Match
Best Local Similarity 82.4%; Score 56; DB 2; Length 145;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy      1 CFCXXXDRIGXXSXXC 17
      ||| ||| ||| |||
Db      125 CFCGRMDRIGSWSLGC 141

RESULT 16
Q7T102_ORYLA PRELIMINARY; PRT; 146 AA.
ID Q7T102_ORYLA PRELIMINARY; PRT; 146 AA.
AC Q7T102;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE B-type natriuretic peptide.
GN Name=bnp;
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OC NCBI_TaxID=8090;
OX NCBI_TaxID=8090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RA Inoue K., Takei Y.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB097900; BAC79151.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002406; C_natriurecep.
DR InterPro; IPR000663; Natri_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRODOM; PD005617; Natri_peptide.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasactive.
SQ SEQUENCE 146 AA; 16455 MW; E0EA2C0C70DAD51F CRC64;

Query Match      82.4%; Score 56; DB 2; Length 146;
Best Local Similarity 58.8%; Pred. No. 0.00059;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      1 CFCXXXDRIGXXSXXC 17
      ||| ||| ||| |||
Db      121 CFCGRMDRIGSWSLGC 137

RESULT 17
ANPB ACITR STANDARD; PRT; 150 AA.
ID ANPB ACITR STANDARD; PRT; 150 AA.
AC P83965;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Brain natriuretic peptide precursor (B-type natriuretic peptide).
GN Name=bnp;
OS Acipenser transmontanus (White sturgeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae;
OC Acipenser.
OX NCBI_TaxID=7904;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND TISSUE SPECIFICITY.
RC TISSUE=Heart ventricle;
RA PubMed=15072558; DOI=10.1677/jme.0.0320547;
RA Kawakoshi A., Hyodo S., Inoue K., Kobayashi Y., Takei Y.;
RA "Four natriuretic peptides (ANP, BNP, VNP and CNP) coexist in the
RT sturgeon: identification of BNP in fish lineage.";
RL J. Mol. Endocrinol. 32:547-555(2004).
-i- FUNCTION: Acts as a cardiac hormone with a variety of biological

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CC actions including natriuretic, diuretic, vasorelaxation, and
CC inhibition of renin and aldosterone secretion. It is thought to
CC play a key role in cardiovascular homeostasis. Helps restore the
CC body's salt and water balance. Improves heart function.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Atrium and ventricle, and to a lesser extent
CC in brain.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AB087729; BAD02836.1; -; mRNA.
DR InterPro; IPR002408; Br_natriurecep.
DR InterPro; IPR000663; Natri_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR PRODOM; PD005617; Natri_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Hormone; Signal; Vasactive; Potential.
FT SIGNAL 1 25
FT PROPEP 26 ?
FT PEPTIDE 130 Brain natriuretic peptide.
FT DISULFID 123 139 By similarity.
SQ SEQUENCE 150 AA; 16758 MW; AD5AA59C0BC292AB CRC64;

Query Match      82.4%; Score 56; DB 1; Length 150;
Best Local Similarity 58.8%; Pred. No. 0.00061;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      1 CFCXXXDRIGXXSXXC 17
      ||| ||| ||| |||
Db      123 CFCGRMDRIGSWSLGC 139

RESULT 18
Q90X61 BUFMA PRELIMINARY; PRT; 159 AA.
ID Q90X61 BUFMA PRELIMINARY; PRT; 159 AA.
AC Q90X61;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Atrial natriuretic peptide.
GN Name=ANP;
OS Bufo marinus (Giant toad) (Cane toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Bufonidae; Bufo.
OX NCBI_TaxID=8386;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22489717; PubMed=12601618; DOI=10.1086/344740;
RA Donald J.A., Meier S.K., Riddell S.;
RT "Toad atrial natriuretic peptide: cDNA cloning and functional analysis
RT in isolated perfused kidneys.";
RL Physiol. Biochem. Zool. 75:617-626(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Donald J.A., Riddell S.;
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF429999; AAL27433.3; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007582; P:physiological process; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
KW Vasactive.
SQ SEQUENCE 159 AA; 17418 MW; 0C06AEF07E12131A CRC64;

Query Match      82.4%; Score 56; DB 2; Length 159;

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Best Local Similarity 58.8%; Pred. No. 0.00064;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFCXXXDRIGXXSXXGC 17
DB 128 CFCGRIDRIGAGSGMGC 144

RESULT 19

ANFC_CHICK
ID ANFC_CHICK STANDARD; PRT; 22 AA.
AC P21805;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-type natriuretic peptide (CNP).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archaeopteryx; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP PROTEIN SEQUENCE.
RC MEDLINE=9113186; PubMed=1989595;
RA Arimura J.J., Minamino N., Kangawa K., Matsuo H.;
RT "Isolation and identification of C-type natriuretic peptide in chicken brain."
RL Biochem. Biophys. Res. Commun. 174:142-148 (1991).
CC -1- FUNCTION: Vasorelaxant activity. Has a GMP-stimulating activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC PIR; J0581; J0581.
DR Ensembl; ENSGALG0000004572; Gallus gallus.
DR InterPro; IPR002408; Br_natriureticpep.
DR InterPro; IPR000663; Natri_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR PRODOM; PD005617; Natri_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Direct protein sequencing; Hormone; Vasoreactive.
FT DISULFID 6 22
SQ SEQUENCE 22 AA; 2244 MW; FC2A4706D8DAC025 CRC64;

Query Match 80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFCXXXDRIGXXSXXGC 17
DB 6 CFCGLKDRIGSMGSLGC 22

RESULT 20

Q4SND6_TETNG PRELIMINARY; PRT; 25 AA.
AC Q4SND6;
DT 13-SEP-2005 (TREMBLREL. 31, Created)
DT 13-SEP-2005 (TREMBLREL. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLREL. 31, Last annotation update)
DE Chromosome 8 SCAR14543, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=STENG00015340001;

OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Arny J.M., Brunet F., Petit J.L., Strange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dosat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castell V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Catolico L., Poulain J., De Bernardis V.,
RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volt J.N., Galgo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957 (2004).
RN [2]

RP NUCLEOTIDE SEQUENCE.
RG Genoscope, Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB0104543; CAP97846.1; -; Genomic_DNA.
DR InterPro; IPR002408; Br_natriureticpep.
DR InterPro; IPR000663; Natri_peptide.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR PRODOM; PD005617; Natri_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoreactive.

FT NON_TER 1 1
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2727 MW; 8D77FED313F74A90 CRC64;

Query Match 80.9%; Score 55; DB 2; Length 25;
Best Local Similarity 58.8%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFCXXXDRIGXXSXXGC 17
DB 9 CFCGLKDRIGSMGSLGC 25

RESULT 21

ANF_ANGJA
ID ANF_ANGJA STANDARD; PRT; 27 AA.
AC P18144;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Atrial natriuretic factor (ANF) (Atrial natriuretic peptide) (ANP).
OS Anguilla japonica (Japanese eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguilla.
OX NCBI_TaxID=7937;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Heart atrium;
RX MEDLINE=90026430; PubMed=2529857;
RA Takei Y., Takahashi A., Watanabe T.X., Nakajima K., Sakakibara S.,
RT "Amino acid sequence and relative biological activity of eel atrial
RT natriuretic peptide.";
RL Biochem. Biophys. Res. Commun. 164:537-543 (1989).

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CC -1- FUNCTION: A potent vasoactive substance which is thought to play a
CC key role in cardiovascular homeostasis. Has a cGMP-stimulating
CC activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR: A33431; A33431.
CC InterPro: IPR002407; At_natriurtcep.
CC InterPro: IPR002408; Br_natriurtcep.
CC InterPro: IPR000663; Natr_peptide.
CC PANTHER: PTHR11415; At_natriurtcep; 1.
CC Pfam: PF00212; ANP; 1.
CC PRINTS: PR00712; BNATPEPTIDE.
CC PRINTS: PR00710; NATPEPTIDES.
CC ProDom: PD005107; At_natriurtcep; 1.
CC ProDom: PD005617; Natr_peptide; 2.
CC SMART: SM00183; NAT_PEP; 1.
CC PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
CC Direct protein sequencing; Hormone; Vasoactive.
KW DISULFID
FT SEQUENCE 27 AA; 2792 MW; 9EF510CCF282B4D CRC64;

Query Match 80.9%; Score 55; DB 1; Length 27;
Best Local Similarity 58.8%; Pred. No. 0.00021;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17
Db 7 CFGKLDRIIGSYGLGC 23

RESULT 22
Q9Q296_CAVPO PRELIMINARY; PRT; 33 AA.
AC Q9Q296;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-type natriuretic peptide/factor (fragment).
GN Name=CNP;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniala; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Harley; TISSUE=Heart;
RA Aguan K., Thompson L., Weiner C.P.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; A193572; AAF04122.1; -, mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro: IPR002408; Br_natriurtcep.
DR InterPro: IPR002406; C_natriurtcep.
DR InterPro: IPR000663; Natr_peptide.
DR Pfam: PF00212; ANP; 1.
DR PRINTS: PR00712; BNATPEPTIDE.
DR PRINTS: PR00710; NATPEPTIDES.
DR PRINTS: PR00710; NATPEPTIDES.
DR ProDom: PD005617; Natr_peptide; 1.
DR SMART: SM00183; NAT_PEP; 1.
DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
FT CHAIN <1 33 C-type natriuretic peptide/factor active
peptide.

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FT NON_TER 1 1
SQ SEQUENCE 33 AA; 3445 MW; C4DE805DF7E762AE CRC64;

Query Match 80.9%; Score 55; DB 2; Length 33;
Best Local Similarity 58.8%; Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17
Db 17 CFGKLDRIIGSYGLGC 33

RESULT 23
NPNP_PSEPC
ID NPNP_PSEPC STANDARD; PRT; 37 AA.
AC P82972;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Natriuretic peptide PNP.
OS Pseudocerastes persicus (Persian horned viper) (False horned viper).
OC Eukaryota; Metazoa; Chordata; Craniala; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Viperinae; Pseudocerastes.
OX NCBI_TaxID=47769;
RN [1]
RP PROTEIN SEQUENCE, FUNCTION, SUBUNIT, SUBCELLULAR LOCATION, TISSUE
RP SPECIFICITY, MASS SPECTROMETRY, AND DISULFIDE BOND.
RC TISSUE=Venom;
RX PubMed=14741349; DOI=10.1016/S0014-5793(03)01455-8;
RA Amlinaasab M., Elmi M.M., Endlich N., Parekh N.,
RA Naderi-Manesh H., Schaller J., Mostafavi H., Sattler M.,
RA Sarbolouki M.N., Muhle-Goll C.;
RT "Functional and structural characterization of a novel member of the
RT natriuretic family of peptides from the venom of Pseudocerastes
RT persicus.";
RL FEBS Lett. 557:104-108(2004).
CC -1- FUNCTION: Increases urine flow and decreases blood pressure when
CC administered to rats by intravenous injection. Inhibits thrombin-
CC induced platelet aggregation. Has a cGMP-stimulating activity.
CC -1- SUBUNIT: Monomer. Binds to the NPR-A receptor.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- MASS SPECTROMETRY: MW=3941.5; MW_ERR=0.17; METHOD=Electrospray;
CC RANGE=1-37; NOT=Ref.1.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC GO; GO:0005576; C:extracellular region; IDA.
CC GO; GO:0030146; P:negative regulation of blood pressure; IDA.
CC GO; GO:0045776; P:negative regulation of blood pressure; IDA.
CC GO; GO:0009405; P:pachyogenesis; IDA.
CC GO; GO:0030828; P:positive regulation of cGMP biosynthesis; IDA.
CC InterPro: IPR002407; At_natriurtcep.
CC InterPro: IPR002408; Br_natriurtcep.
CC InterPro: IPR000663; Natr_peptide.
CC Pfam: PF00212; ANP; 1.
CC PRINTS: PR00712; BNATPEPTIDE.
CC PRINTS: PR00710; NATPEPTIDES.
CC ProDom: PD005107; At_natriurtcep; 1.
CC ProDom: PD005617; Natr_peptide; 1.
CC SMART: SM00183; NAT_PEP; 1.
CC PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
KW Direct protein sequencing; Toxin; Vasoactive.
KW DISULFID 14 30
FT SEQUENCE 37 AA; 3944 MW; AD7BE649AD480BA6 CRC64;

Query Match 80.9%; Score 55; DB 1; Length 37;

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Best Local Similarity 58.8%; Pred. No. 0.00028;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFCGXXDRIGXXSXXGC 17
14 CFCGKIDRIGSHSGGCG 30

Db 14 CFCGKIDRIGSHSGGCG 30

RESULT 24
Q7LZ09_VIPLE PRELIMINARY; PRT; 38 AA.

AC 07LZ09;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Lebetin 2 isoform alpha.
OS Vipera lebetina (Elephant snake) (Leventine viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Viperinae; Macrovipera.
OX NCBI_Taxid=8709;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=96354866; PubMed=8769304; DOI=10.1016/0014-5793(96)00774-0;
RA Barhouche R., Marakchi N., Manuelle P., Kifli M., Fenouillet E.,
RA Rochat H., El Ayeb M.;
RT "Novel anti-platelet aggregation polypeptides from Vipera lebetina
venom: Isolation and characterization.";
RL FEBS Lett. 392:6-10(1996).
DR PIR, S71381; S71381.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; P:hormone activity; IEA.
DR GO; GO:0058880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002408; B: Natr_turtcpep.
DR InterPro; IPR000663; B: Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR Prodom; PD005617; Natr_peptide; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasactive.
SQ SEQUENCE 38 AA; 3945 MW; 831FA5C9B1B09377 CRC64;

Query Match 80.9%; Score 55; DB 2; Length 38;
Best Local Similarity 58.8%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFCGXXDRIGXXSXXGC 17
14 CFCGKIDRIGSHSGGCG 30

Db 14 CFCGKIDRIGSHSGGCG 30

RESULT 25
Q4S797_TETNG PRELIMINARY; PRT; 101 AA.

AC 04S797;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Chromosome 1 SCAFI4716, whole genome shotgun sequence.
GN ORFNames=GSTENG00022908001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_Taxid=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Arny J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bounoue L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicud S., Jaffe D., Fieber S., Lutfalla G., Dossat C., Segreus B.,
RA Desliva C., Salanoubat M., Levy M., Boudet N., Castellano S.,

RA Anthonard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Catolico L., Poulain J., De Bernardis V.,
RA Crnaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McSwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lauder V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAE01014716; CAG03485.1; -; Genomic DNA.
DR InterPro; IPR002406; C_natrurtcpep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR Prodom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasactive.
SQ SEQUENCE 101 AA; 11398 MW; 31CA29F92812C3D0 CRC64;

Query Match 80.9%; Score 55; DB 2; Length 101;
Best Local Similarity 58.8%; Pred. No. 0.0007;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFCGXXDRIGXXSXXGC 17
85 CFCGKMDRIGTISGMGC 101

Db 85 CFCGKMDRIGTISGMGC 101

RESULT 26
ANFB_BOVIN STANDARD; PRT; 103 AA.

AC P13204;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Natriuretic peptides B precursor (Contains: Gamma-brain natriuretic
DE peptide; Aldosterone secretion inhibitory factor (ASIF); Brain
DE natriuretic peptide 26 (BNP-26)).
CN Name=NPBP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=90114187; PubMed=2532709;
RA Nguyen T.T., Lazure C., Babinski K., Chretien M., de Lean A., Ong H.;
RT "Purification and primary structure of pro-aldosterone secretion
RT inhibitory factor from bovine adrenal chromaffin cells.";
RL Mol. Endocrinol. 3:1823-1829(1989).
RN [2]
RP PROTEIN SEQUENCE OF 69-103.
RX MEDLINE=89136947; PubMed=2537187;
RA Nguyen T.T., Lazure C., Babinski K., Chretien M., Ong H., de Lean A.;
RT "Aldosterone secretion inhibitory factor: a novel neuropeptide in
RL bovine chromaffin cells.";
RL Endocrinology 124:1591-1593(1989).
CC -!- FUNCTION: Acts as a cardiac hormone with a variety of biological
CC actions including natriuresis, diuresis, vasorelaxation, and
CC inhibition of renin and aldosterone secretion. It is thought to
CC play a key role in cardiovascular homeostasis. Helps restore the

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CC      body's salt and water balance. Improves heart function.
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- TISSUE SPECIFICITY: Brain and also in atria, but at much lower
CC      levels than ANP.
CC      -1- SIMILARITY: Belongs to the natriuretic peptide family.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      PIR: A41403; A41403.
CC      InterPro: IPR002408; Br_natriurtcp.
CC      InterPro: IPR000663; Natr_peptide.
CC      Pfam: PF00212; ANP; 1.
CC      PRINTS: PR00712; BNATPEPTIDE.
CC      PRINTS: PR00710; NATPEPTIDES.
CC      ProDom: PD005617; Natr_peptide; 1.
CC      PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
CC      Direct protein sequencing; Hormone; Vasoactive.
CC      CHAIN
CC      FT CHAIN 1 103 Gamma-brain natriuretic peptide.
CC      PEPTIDE 69 103 Aldosterone secretion inhibitory factor.
CC      FT PEPTIDE 78 103 Brain natriuretic peptide 26.
CC      DISULFID 81 97
CC      FT DISULFID 81 97
CC      SQ SEQUENCE 103 AA; 11249 MW; 40209204AFB3651D CRC64;

Query Match
Best Local Similarity 80.9%; Score 55; DB 1; Length 103;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXGC 17
DB      81 CFGRLDRIGSLGSGC 97

RESULT 27
Q9GLK5_FELCA PRELIMINARY; PRT; 112 AA.
ID Q9GLK5;
AC Q9GLK5;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Brain natriuretic peptide (Fragment).
OS Fells silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Fells.
OC NCBI_TaxId=9685;
OK
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Liu Z.T., Wiedmeyer C.E., Solter P.F., Sisson D.D.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF251261; AAG13660.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro: IPR002408; Br_natriurtcp.
DR InterPro: IPR000663; Natr_peptide.
DR Pfam: PF00212; ANP; 1.
DR PRINTS: PR00712; BNATPEPTIDE.
DR PRINTS: PR00710; NATPEPTIDES.
DR ProDom: PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
FT NON_TER 1 1
FT SEQUENCE 112 AA; 12083 MW; 580224F12964FFB2 CRC64;

Query Match
Best Local Similarity 80.9%; Score 55; DB 2; Length 112;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY      1 CFGXXXDRIGXXSXGC 17
DB      90 CFGRLDRIGSLGSGC 106

RESULT 28
ANFC_SCYCA STANDARD; PRT; 115 AA.
ID ANFC_SCYCA
AC P23259;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE C-type natriuretic peptide prohormone precursor (CNP-115) [Contains:
DE CNP-39; CNP-38; CNP-22].
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphi; Galeidae; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OK
RN NCBI_TaxId=7830;
RN [1]
RP PROTEIN SEQUENCE.
RA TISSUE-Heart atrium, and Heart ventricle;
RA MEDLINE=91243822; PubMed=1828036; DOI=10.1016/0014-5793(91)80505-W;
RA Suzuki R., Takahashi A., Hazon N., Takei Y.;
RT "Isolation of high-molecular-weight C-type natriuretic peptide from
RT the heart of a cartilaginous fish (European dogfish, Scyliorhinus
RT canicula)."
RL FEBS Lett. 282:321-325(1991).
CC -1- FUNCTION: Vasoorelaxant activity. Has a cGMP-stimulating activity
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: CNP-115 is differentially processed to produce
CC CNP-38 and CNP-39 in the heart and CNP-22 in the brain.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      PIR: S15822; S15822.
CC      InterPro: IPR002406; C_natriurtcp.
CC      InterPro: IPR000663; Natr_peptide.
CC      Pfam: PF00212; ANP; 1.
CC      PRINTS: PR00713; CNATPEPTIDE.
CC      PRINTS: PR00710; NATPEPTIDES.
CC      ProDom: PD005617; Natr_peptide; 1.
CC      SMART; SM00183; NAT_PEP; 1.
CC      PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
CC      Direct protein sequencing; Hormone; Vasoactive.
CC      CHAIN
CC      FT CHAIN 1 115 C-type natriuretic peptide prohormone.
CC      PEPTIDE 77 115 CNP-39.
CC      FT PEPTIDE 78 115 CNP-38.
CC      FT PEPTIDE 94 115 CNP-22.
CC      FT DISULFID 99 115 By similarity.
CC      SQ SEQUENCE 115 AA; 12885 MW; 49AE7200EE4C7F8A CRC64;

Query Match
Best Local Similarity 80.9%; Score 55; DB 1; Length 115;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXGC 17
DB      99 CFGVLDRIIGSLGSGC 115

RESULT 29
ANFD_RANCA STANDARD; PRT; 118 AA.
ID ANFD_RANCA
AC P40756;
DT 01-FEB-1995 (Rel. 31, Created)

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DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DE 10-MAY-2005 (Rel. 47, Last annotation update)
 DR C-type natriuretic peptide-2 precursor (CNP II).
 OS Rana catesbeiana (Bull Frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana;
 CC Aquarana.
 OC NCBI_TaxID=8400;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RA MEDLINE=94230409; PubMed=8175740;
 RT Kojima M., Ohyama Y., Miyamoto K., Minamino N., Kangawa K., Matsuo H.;
 RT "Cloning and characterization of a novel natriuretic peptide in frog
 (Rana catesbeiana)."
 RU J. Biol. Chem. 269:11136-11140(1994).
 CC -1- FUNCTION: Exhibits natriuretic and vasodepressor activity. Has a
 CC GMP-stimulating activity.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL: D17414; BAA04236.1; -; mRNA.
 DR PIR: B54119; B54119.
 DR InterPro: IPR002406; C_natriureticpep.
 DR InterPro: IPR000663; Natr_peptide.
 DR Pfam: PF00212; ANP; 1.
 DR PRINTS: PR00713; CNATPEPTIDE.
 DR PRODOM: PD005617; Natriuretic_Peptide; 1.
 DR SMART: SM00183; NAT_PEP; 1.
 DR PROSITE: PS00263; NATRIURETIC_PEP; 1.
 KW Hormone; Signal; Vasoactive.
 FT SIGNAL 1 22 Potential.
 FT PROPEP 23 94
 FT PEPTIDE 97 118 C-type natriuretic peptide-2.
 FT DISULFID 102 118 By similarity.
 SQ SEQUENCE 118 AA; 13136 MW; F091C3C4AD707603 CRC64;
 Query Match 80.9%; Score 55; DB 1; Length 118;
 Best Local Similarity 58.8%; Pred. No. 0.00081;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 Oy 1 CFGXXXDRIGXXSXGC 17
 Db 102 CFGKLDRIIGMSGIGC 118

RT "Four functionally distinct C-type natriuretic peptides found in fish
 RT reveal evolutionary history of the natriuretic peptide system.";
 RU Proc. Natl. Acad. Sci. U.S.A. 100:10079-10084(2003).
 CC -1- FUNCTION: Exhibits natriuretic and vasodepressor activity. Has
 CC GMP-stimulating activity. May help to regulate body fluid
 CC homeostasis in a variety of aquatic environments.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL: AB089938; BAC57074.1; -; mRNA.
 DR Ensemble: SINEFUG00000151691; Fugu rubripes.
 DR InterPro: IPR002406; C_natriureticpep.
 DR InterPro: IPR000663; Natr_peptide.
 DR Pfam: PF00212; ANP; 1.
 DR PRINTS: PR00713; CNATPEPTIDE.
 DR PRODOM: PD005617; Natriuretic_Peptide; 1.
 DR SMART: SM00183; NAT_PEP; 1.
 DR PROSITE: PS00263; NATRIURETIC_PEP; 1.
 KW Hormone; Signal; Vasoactive.
 FT SIGNAL 1 22 Potential.
 FT PROPEP 23 94
 FT PEPTIDE 97 120 C-type natriuretic peptide-4.
 FT DISULFID 104 120 By similarity.
 SQ SEQUENCE 120 AA; 13504 MW; 27233ABCI3FA3113E CRC64;
 Query Match 80.9%; Score 55; DB 1; Length 120;
 Best Local Similarity 58.8%; Pred. No. 0.00082;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 Oy 1 CFGXXXDRIGXXSXGC 17
 Db 104 CFGHMDRIIGTISGMGC 120

RESULT 31
 ANFB MOUSE STANDARD; PRT; 121 AA.
 AC P40753;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE 10-MAY-2005 (Rel. 47, Last annotation update)
 DR Natriuretic peptide B precursor [Contains: Gamma-brain natriuretic
 DE peptide; Brain natriuretic peptide (BNP)].
 GN Name=Nppb;
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 CC Muridae; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/c; TISSUE=Heart;
 RX MEDLINE=94237953; PubMed=8182124;
 RA Ogawa Y., Itoh H., Tamura N., Suga S., Yoshimasa T., Uehira M.,
 RA Matsuda S., Shiono S., Nishimoto H., Nakao K.;
 RT "Molecular cloning of the complementary DNA and gene that encode mouse
 RT brain natriuretic peptide and generation of transgenic mice that
 RT overexpress the brain natriuretic peptide gene.";
 RL J. Clin. Invest. 93:1911-1921(1994).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/c;
 RX MEDLINE=93238395; PubMed=8097440;
 RA Steinleider M.E.;
 RT "Structure, expression, and genomic mapping of the mouse natriuretic
 RT peptide type-B gene.";

RL Circ. Res. 72:984-992(1993).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LONG).
 RC TISSUE=Testis;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millhys S.J.,
 RA Boask S.A., McEwan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richard S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Acts as a cardiac hormone with a variety of biological
 CC actions including natriuresis, diuresis, vasorelaxation, and
 CC inhibition of renin and aldosterone secretion. It is thought to
 CC play a key role in cardiovascular homeostasis. Helps restore the
 CC body's salt and water balance. Improves heart function.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoId=PA0753-1; Sequence=Displayed;
 CC Name=Short;
 CC IsoId=PA0753-2; Sequence=VSP_000263;
 CC -1- TISSUE SPECIFICITY: Expressed abundantly in the ventricle, and in
 CC a lesser extent in the atrium.
 CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: D16497; BAA03948.1; -; Genomic DNA.
 CC EMBL: S58667; AAB26344.2; -; Genomic DNA.
 CC EMBL: BC061165; AAH61165.1; -; mRNA.
 CC FIR: 149548; 149548.
 CC Ensembl: ENSMUSG00000029019; Mus musculus.
 CC MGI: 97368; Npbp.
 CC GO: GO:0005615; Extracellular space; TAS.
 CC InterPro: IPR002408; Br_natriurecep.
 CC InterPro: IPR000663; Natr_peptide.
 CC Pfam: PF00212; ANP; 1.
 CC PRINTS: PR00712; BNATPEPTIDE.
 CC PRODOM: PD005617; Natr_peptide; 1.
 CC PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
 CC Alternative splicing; Hormone; Signal; Vasoactive.
 CC KM SIGNAL 1
 CC FT PEPTIDE 1 26 By similarity.
 CC FT PEPTIDE 121 Gamma-brain natriuretic peptide.
 CC FT PEPTIDE 77 121 Brain natriuretic peptide.
 CC FT DISULFID 99 115 By similarity.
 CC FT VARSPPLIC 43 43 Missing (in isoform Short).
 CC FT VARSPPLIC 43 43 /FTId=VSP_000263.
 CC FT CONFLICT 27 27 Y -> H (in Ref. 2).
 CC FT CONFLICT 71 71 P -> L (in Ref. 2).
 CC SQ SEQUENCE 121 AA; 13756 MW; 4F62AC9445B293B9 CRC64;
 CC Query Match 80.9%; Score 55; DB 1; Length 121;

Best Local Similarity 58.8%; Pred. No. 0.00083;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CFFXXXXRIKXXSXGCC 17
 DB 99 CFFHKRIDIGSVSRIGC 115
 RESULT 32
 ANFB_RAT
 ID ANFB_RAT STANDARD; PRT; 121 AA.
 AC P13205;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Natriuretic peptides B precursor (iso-ANP) [Contains: Gamma-brain
 DE natriuretic peptide; Brain natriuretic peptide 45 (BNP-34) (5 kDa
 DE cardiac natriuretic peptide)].
 GN Name=Npbp;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=89193742; PubMed=2522776;
 RA Kojima M., Minamino N., Kangawa K., Matsuo H.,
 RT "Cloning and sequence analysis of cDNA encoding a precursor for rat
 RT brain natriuretic peptide.";
 RL Biochem. Biophys. Res. Commun. 159:1420-1426(1989).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=90365739; PubMed=2144113;
 RA Roy R.N., Flynn T.G.,
 RT "Organization of the gene for iso-rANP, a rat B-type natriuretic
 RT peptide.";
 RL Biochem. Biophys. Res. Commun. 171:416-423(1990).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92123224; PubMed=1837590;
 RA Dagnino L., Drouin J., Nemer M.,
 RT "Differential expression of natriuretic peptide genes in cardiac and
 RT extracardiac tissues.";
 RL Mol. Endocrinol. 5:1292-1300(1991).
 RN [4]
 RP PROTEIN SEQUENCE OF 27-121.
 RX MEDLINE=89374230; PubMed=2673236;
 RA Abuyara M., Hino J., Minamino N., Kangawa K., Matsuo H.,
 RT "Isolation and identification of rat brain natriuretic peptides in
 RT cardiac atrium.";
 RL Biochem. Biophys. Res. Commun. 163:226-232(1989).
 RN [5]
 RP PROTEIN SEQUENCE OF 77-121.
 RC TISSUE=Heart;
 RX MEDLINE=89374231; PubMed=2528349;
 RA Kambayashi Y., Nakao K., Itoh H., Hosoda K., Saito Y., Yamada T.,
 RA Mukoyama M., Arai H., Shirikami G., Suga S.-I., Ogawa Y.,
 RA Jougasaki M., Minamino N., Kangawa K., Matsuo H., Imura H.,
 RT "Isolation and sequence determination of rat cardiac natriuretic
 RT peptide.";
 RL Biochem. Biophys. Res. Commun. 163:233-240(1989).
 RN [6]
 RP PROTEIN SEQUENCE OF 77-121.
 RX MEDLINE=89286593; PubMed=2525380;
 RA Flynn T.G., Brar A., Tremblay L., Sarda I., Lyons C., Jennings D.B.,
 RT "Isolation and characterization of iso-rANP, a new natriuretic peptide
 RT from rat atria.";
 RL Biochem. Biophys. Res. Commun. 161:830-837(1989).
 RN [7]
 RP PROTEIN SEQUENCE OF 99-115.
 RX MEDLINE=89286579; PubMed=2525379;
 RA Itoh H., Nakao K., Kambayashi Y., Hosoda K., Saito Y., Yamada T.,

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RA Mukoyama M., Arai H., Shirakami G., Suga S.-I., Yoshida I., Inouye K.,
RA Imura H.;
RT "Occurrence of a novel cardiac natriuretic peptide in rats."
RL Biochem. Biophys. Res. Commun. 161:732-739(1989).
CC -1- FUNCTION: Acts as a cardiac hormone with a variety of biological
CC actions including natriuresis, diuresis, vasorelaxation, and
CC inhibition of renin and aldosterone secretion. It is thought to
CC play a key role in cardiovascular homeostasis. Helps restore the
CC body's salt and water balance. Improves heart function.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Brain and also in atria, but at much lower
CC levels than ANP.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL, M25297; AA57269.1; -; mRNA.
DR EMBL, M60731; AA41456.1; -; Genomic DNA.
DR EMBL, M60266; AA41455.1; -; Genomic DNA.
DR PIR, A30162; A30162.
DR Ensemble; ENSRNOG00000008141; Rattus norvegicus.
DR RGD, 3194; Nppb.
DR InterPro; IPR002408; Br_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KM Direct protein sequencing; Hormone; Signal; Vasocactive.
FT SIGNAL 1 26
FT PEPIDE 27 121 Gamma-brain natriuretic peptide.
FT PEPIDE 77 121 Brain natriuretic peptide 45.
FT DISULFID 99 115 L -> V (in Ref. 2).
FT CONFLICT 15 15 L -> Q (in Ref. 6).
FT CONFLICT 120 120
SQ SEQUENCE 121 AA; 13656 MW; B5D4151ED18C7294 CRC64;

Query Match 80.9%; Score 55; DB 1; Length 121;
Best Local Similarity 58.8%; Pred. No. 0.00083;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXXRIGXXXXXC 17
DB 99 CFGQKIDRIGAVSRIGC 115

RESULT 33
ANFCA_ORYLA STANDARD; PRT; 121 AA.
ID ANFCA_ORYLA STANDARD; PRT; 121 AA.
AC 080017;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide-4 precursor.
GN Name=cnp-4;
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorphi; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziatidae; Oryzias.
OC NCBI_TaxID=8090;
OX NCBI_TaxID=8090;
RN [1]
RP NUCLEOTIDE SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND SYNTHESIS.
RC TISSUE=Brain;
RA PubMed:12633874; DOI=10.1073/pnas.1632366100; Suzuki N., Takei Y.,
RA Inoue K., Naruse K., Yamagami S., Mitani H.,
RT "Four functionally distinct C-type natriuretic peptides found in fish
RT reveal evolutionary history of the natriuretic peptide system.";
```

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RL Proc. Natl. Acad. Sci. U.S.A. 100:10079-10084(2003).
CC -1- FUNCTION: Exhibits natriuretic and vasodepressant activity. Has
CC CGMP-stimulating activity. May help to regulate body fluid
CC homeostasis in a variety of aquatic environments.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Brain, spinal cord, spleen, heart and fin, and
CC to a lower extent in gill and ovary.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL, AB091699; BAC65998.1; -; mRNA.
DR InterPro; IPR002408; Br_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KM Hormone; Signal; Vasocactive.
FT SIGNAL 1 22 Potential.
FT PROPEP 23 94 By similarity.
FT PEPIDE 97 121 C-type natriuretic peptide-4.
FT DISULFID 105 121 By similarity.
SQ SEQUENCE 121 AA; 13457 MW; EFD7FD534B137009 CRC64;

Query Match 80.9%; Score 55; DB 1; Length 121;
Best Local Similarity 58.8%; Pred. No. 0.00083;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXXRIGXXXXXC 17
DB 105 CFGHMDRIGTISGMC 121

RESULT 34
O794A8 MOUSE
ID O794A8 MOUSE PRELIMINARY; PRT; 121 AA.
AC O794A8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Brain natriuretic peptide.
GN Name=BNP;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HMI/MsT;
RA Liu Y., Kitano T., Koide T., Shiroishi T., Moriaki K., Saitou N.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL, AB039051; BAB68575.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005178; F:hormone activity; IEA.
DR GO; GO:0050880; F:regulation of blood vessel size; IEA.
DR InterPro; IPR002408; Br_natriurtcep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KM Vasocactive.
SQ SEQUENCE 121 AA; 13739 MW; BD608CB65CDB83AA CRC64;
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Query Match      80.9%; Score 55; DB 2; Length 121;
Best Local Similarity 58.8%; Pred. No. 0.00083;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY      1 CFCGXXDRIGXXSXGC 17
      ||| ||| ||| |||
      99 CFCGKIDRIGSVRLGC 115

RESULT 35
O91V40 MUSEI
ID O91V40 MUSEI PRELIMINARY; PRT; 121 AA.
AC O91V40;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Brain natriuretic peptide.
GN Name=BNP;
OS Mus epiclegus (Steppe mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ZBN;
RL Liu Y., Kitano T., Koide T., Shirotshi T., Moriaki K., Saitou N.;
   Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB039053; BAB68577.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; P:hormone activity; IEA.
DR GO; GO:0050880; P:regulation of blood vessel size; IEA.
DR InterPro; IPR002408; Br_natriureticp.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRODOM; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasocactive.
SQ SEQUENCE 121 AA; 13739 MW; BD608C965CDB83AA CRC64;

Query Match      80.9%; Score 55; DB 2; Length 121;
Best Local Similarity 58.8%; Pred. No. 0.00083;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY      1 CFCGXXDRIGXXSXGC 17
      ||| ||| ||| |||
      99 CFCGKIDRIGSVRLGC 115

DB      99 CFCGKIDRIGSVRLGC 115

RESULT 36
O54AE9 MUSEI
ID O54AE9 MUSEI PRELIMINARY; PRT; 121 AA.
AC O54AE9;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Brain natriuretic peptide (adult male heart cDNA, RIKEN full-length
   enriched library, clone:1010001K23 product:natriuretic peptide type B,
   full insert sequence).
GN Name=Nppb; Synonyms=BNP;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CAS/El. NUI/Maf, and C57BL/10SnJ;
RL Liu Y., Kitano T., Koide T., Shirotshi T., Moriaki K., Saitou N.;

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RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RT Five Mus musculus subspecies":
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN (2)
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44 (1999).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner T., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guelincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohatsu S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 403:685-690 (2001).
RN [4]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Otsu N., Saito R., Suzuki H., Yamataka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Brad D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Guelincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kongawa A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Nunata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zevolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imorani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
RN [5]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

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RT "Four functionally distinct C-type natriuretic peptides found in fish
RT reveal evolutionary history of the natriuretic peptide system.";
CC Proc. Natl. Acad. Sci. U.S.A. 100:10079-10084(2003).
CC -1- FUNCTION: Exhibits natriuretic and vasodilator activity. Has
CC CGMP-stimulating activity. May help to regulate body fluid
CC homeostasis in a variety of aquatic environments.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AB089935; BAC57071.1; -; mRNA.
DR Ensembl; SINFUG00000146920; Fugu rubripes.
DR InterPro; IPR002406; C_natriureticp.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
DR Hormone; Signal; Vasoactive.
DR KMW; 1.
DR SIGNAL; 1.
DR PROPEP; 23 102 By similarity.
DR PEPTIDE; 105 126 C-type natriuretic peptide-1.
DR DISULFID; 110 126 By similarity.
DR SEQUENCE 126 AA; 14068 MW; DF3F23C2C6D4FF6 CRC64;

Query Match 80.9%; Score 55; DB 1; Length 126;
Best Local Similarity 58.8%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXXXGC 17
Db 110 CFGKMDRIGSISGLGC 126

RESULT 39
ANFC ORYLA STANDARD; PRT; 126 AA.
AC Q8A9K5;
DR 25-OCT-2004 (Rel. 45, Created)
DR 25-OCT-2004 (Rel. 45, Last sequence update)
DR 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide-2 precursor.
GN Namecnp-2;
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OC NCB1_Taxid=8090;
OK [1]
RP NUCLEOTIDE SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND SYNTHESIS.
RC TISSUE=Brain;
RX PubMed=1289387; DOI=10.1073/pnas.1632368100;
RA Inoue K., Naruse K., Yamagami S., Mitani H., Suzuki N., Takei Y.;
RT "Four functionally distinct C-type natriuretic peptides found in fish
RT reveal evolutionary history of the natriuretic peptide system.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:10079-10084(2003).
CC -1- FUNCTION: Exhibits natriuretic and vasodilator activity. Has
CC CGMP-stimulating activity. May help to regulate body fluid
CC homeostasis in a variety of aquatic environments.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Brain and spinal cord.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC use as long as its content is in no way modified and this statement is not
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CC -----
DR EMBL; AB081456; BAC5761.1; -; mRNA.
DR InterPro; IPR002408; Br_natriureticp.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00712; BNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
DR Hormone; Signal; Vasoactive.
DR KMW; 1.
DR SIGNAL; 1.
DR PROPEP; 23 100 By similarity.
DR PEPTIDE; 103 126 C-type natriuretic peptide-2.
DR DISULFID; 110 126 By similarity.
DR SEQUENCE 126 AA; 13400 MW; 9D5D7B8BDEC80F92 CRC64;

Query Match 80.9%; Score 55; DB 1; Length 126;
Best Local Similarity 58.8%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXXXGC 17
Db 110 CFGKMDRIGSISGLGC 126

RESULT 40
ANFC BOVIN STANDARD; PRT; 126 AA.
AC P55206;
DR 01-OCT-1996 (Rel. 34, Created)
DR 01-OCT-1996 (Rel. 34, Last sequence update)
DR 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide precursor (SVSP15) [contains: CNP-22; CNP-
DE 29; CNP-53].
GN Name=NPFC;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OC NCB1_Taxid=9913;
OK [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94280621; PubMed=8011167;
RA Hosang K.K., Scheit K.K.;
RT "cDNA cloning identified a calmodulin-binding protein in bovine
RT seminal plasma as bovine C-type natriuretic peptide.";
RL DNA Cell Biol. 13:409-417(1994).
CC -1- FUNCTION: Vasoconstrictant activity. Has a CGMP-stimulating activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC -----
DR EMBL; Z48477; CAA88369.1; -; mRNA.
DR EMBL; Z48477; CAA88368.1; -; mRNA.
DR InterPro; IPR002406; C_natriureticp.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
DR Hormone; Signal; Vasoactive.
DR KMW; 1.
DR SIGNAL; 1 23 Potential.
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FT PROPEP 24 72 Potential.
RT PEPTIDE 74 126 CNP-53 (By similarity).
FT PEPTIDE 98 126 CNP-29 (By similarity).
FT PEPTIDE 105 126 CNP-22.
FT DISULFID 110 126 By similarity.
SQ SEQUENCE 126 AA; 13291 MW; 31EDF80FA98DD77 CRC64;

Query Match 80.9%; Score 55; DB 1; Length 126;
Best Local Similarity 58.8%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CPGXXXDRIGXXSXGCG 17
Db 110 CPGKLDRIKSGMSGGCG 126

RESULT 41
ANFC_HUMAN STANDARD; PRT; 126 AA.
ID P23582;
AC 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide precursor [Contains: CNP-22; CNP-29; CNP-53].
GN Name=NPPC; Synonyms=CNP2;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91207363; PubMed=2018508;
RA Tawaragi Y., Fuchimura K., Tanaka S., Minamino N., Kangawa K.,
RA Matsuo H.;
RT "Gene and precursor structures of human C-type natriuretic peptide.";
RL Biochem. Biophys. Res. Commun. 175:645-651(1991).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92275775; PubMed=1339402;
RA Ogawa Y., Nakao K., Nakagawa O., Komatsu Y., Hosoda K., Suga S.,
RA Arai H., Nagata K., Yoshida N., Imura H.;
RT "Human C-type natriuretic peptide. Characterization of the gene and
RT peptide.";
RL Hypertension 19:809-813(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheele C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carroll P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzyzinski M.I., Skalska U.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP PROTEIN SEQUENCE OF 98-126.
RX MEDLINE=93112033; PubMed=1472040;
RA Iehizaka Y., Kangawa K., Minamino N., Iehi K., Takano S., Eto T.,

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RA Matsuo H.;
RT "Isolation and identification of C-type natriuretic peptide in human
RT monocytic cell line, THP-1.";
RT Biochem. Biophys. Res. Commun. 189:697-704(1992).
RL Biochem. Biophys. Res. Commun. 189:697-704(1992).
CC -1- FUNCTION: Vasoorelaxant activity. Has a GMP-stimulating activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
-----
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DR EMBL; M64710; AAA35703.1; -; Genomic DNA.
DR EMBL; D90337; BAA14351.1; -; Genomic DNA.
DR EMBL; BC069120; AAH69120.1; -; mRNA.
DR PIR; J10567; AMHUC.
DR PDB; 1JDP; X-ray; H=105-126.
DR Ensembl; ENSG00000163273; Homo sapiens.
DR HGNC; HGNC:7941; NPPC.
DR MIM; 600296; -.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0008217; P:regulation of blood pressure; NAS.
DR GO; GO:0019229; P:regulation of vasoconstriction; NAS.
DR InterPro; IPR002406; C_natriureticp.
DR InterPro; IPR000663; Natri_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natri_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW 3D-structure; Direct protein sequencing; Hormone; Polymorphism;
KW Signal; Vasoactive.
FT SIGNAL 1 23 Potential.
FT PROPEP 24 72
FT PEPTIDE 74 126 CNP-53.
FT PEPTIDE 98 126 CNP-29.
FT PEPTIDE 105 126 CNP-22.
FT DISULFID 110 126 By similarity.
FT VARIANT 82 82 R -> Q (in dbSNP:5267) .
SQ SEQUENCE 126 AA; 13246 MW; 58F6E57668F9A2D CRC64;

Query Match 80.9%; Score 55; DB 1; Length 126;
Best Local Similarity 58.8%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CPGXXXDRIGXXSXGCG 17
Db 110 CPGKLDRIKSGMSGGCG 126

RESULT 42
ANFC_MOUSE STANDARD; PRT; 126 AA.
ID O61839;
AC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide precursor [Contains: CNP-22; CNP-29; CNP-53].
GN Name=Nppc; Synonyms=Cnp;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95213034; PubMed=7698765;

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RA Ogawa Y., Itoh H., Yoshitake Y., Inoue M., Yoshimasa T., Serikawa T.,
RA Nako K.;
RT "Molecular cloning and chromosomal assignment of the mouse C-type
RT natriuretic peptide (CNP) gene (Nppc): comparison with the human CNP
RT gene (NPPC).";
RL Genomics 24:383-387 (1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SV;
RX MEDLINE=97053441; PubMed=8897953;
RA Huang H., Acuff C.G., Steinhilper M.E.;
RT "Isolation, mapping, and regulated expression of the gene encoding
RT mouse C-type natriuretic peptide.";
RL Am. J. Physiol. 271:H1565-H1575 (1996).
CC -1- FUNCTION: Vasorelaxant activity. Has a cGMP-stimulating activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC -----
DR EMBL, D28873; BA06028.1; -; Genomic DNA.
DR EMBL, U62939; AAB61717.1; -; Genomic DNA.
DR PIR, A55688; A55688.
DR Ensembl; ENSMUSG0000026241; Mus musculus.
DR MGI, MGI:97369; Nppc.
DR GO, GO:0005615; C:extracellular space; TAS.
DR GO, GO:0005184; F:neuropeptide hormone activity; TAS.
DR GO, GO:0005102; F:receptor binding; IDA.
DR GO, GO:0006182; P:cGMP biosynthesis; IDA.
DR InterPro; IPR002406; C_natriureticp.
DR InterPro; IPR000663; Natriureticp.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natri_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
DR Hormone; Signal; Vasorelaxant.
DR KMW SIGNAL 1 23 Potential.
FT PROPEP 1 23
FT PEPTIDE 74 72
FT PEPTIDE 74 126 CNP-53 (By similarity).
FT PEPTIDE 98 126 CNP-29 (By similarity).
FT PEPTIDE 105 126
FT DISULFID 110 126 By similarity.
SQ SEQUENCE 126 AA; 13320 MW; 8F65B1C4B82F0ACB CRC64;

Query Match 80.9%; Score 55; DB 1; Length 126;
Best Local Similarity 58.8%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFFGXXXDRIGXXSXXGC 17
Db 110 CFFGLKLDRIGSWSGLGC 126

RESULT 43
ANFC_PIG STANDARD; PRT; 126 AA.
AC P18104; P21806;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide precursor [Contains: CNP-22; CNP-29; CNP-
DE 53].
GN Name=NPPC; Synonyms=CNP;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
OC Sus.

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OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91054475; PubMed=2146957;
RA Tawaragi Y., Fuchimura K., Nakazato H., Tanaka S., Minamino N.,
RA Kanawa K., Matsuo H.;
RT "Gene and precursor structure of porcine C-type natriuretic peptide.";
RL Biochem. Biophys. Res. Commun. 172:627-632 (1990).
RN [2]
RP PROTEIN SEQUENCE OF 74-126.
RC TISSUE=Brain;
RX MEDLINE=90343827; PubMed=2383278;
RA Minamino N., Kanawa K., Matsuo H.;
RT "N-terminally extended form of C-type natriuretic peptide (CNP-53)
RT identified in porcine brain.";
RL Biochem. Biophys. Res. Commun. 170:973-979 (1990).
RN [3]
RP PROTEIN SEQUENCE OF 105-126.
RC TISSUE=Brain;
RX MEDLINE=90241265; PubMed=2139780;
RA Sudoh T., Minamino N., Kanawa K., Matsuo H.;
RT "C-type natriuretic peptide (CNP): a new member of natriuretic peptide
RT family identified in porcine brain.";
RL Biochem. Biophys. Res. Commun. 168:863-870 (1990).
CC -1- FUNCTION: Vasorelaxant activity. Has a cGMP-stimulating activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
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CC -----
DR EMBL, M64758; AAA31018.1; -; Genomic DNA.
DR PIR, A36155; A36155.
DR InterPro; IPR002406; C_natriureticp.
DR InterPro; IPR000663; Natri_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natri_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
DR Direct protein sequencing; Hormone; Signal; Vasorelaxant.
DR KMW SIGNAL 1 23 Potential.
FT PROPEP 1 23
FT PEPTIDE 74 72
FT PEPTIDE 74 126 CNP-53.
FT PEPTIDE 98 126 CNP-29 (By similarity).
FT PEPTIDE 105 126
FT DISULFID 110 126
SQ SEQUENCE 126 AA; 13243 MW; E2474B2D4AABF4DD CRC64;

Query Match 80.9%; Score 55; DB 1; Length 126;
Best Local Similarity 58.8%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFFGXXXDRIGXXSXXGC 17
Db 110 CFFGLKLDRIGSWSGLGC 126

RESULT 44
ANFC_RAT STANDARD; PRT; 126 AA.
AC P55207;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide precursor [Contains: CNP-22; CNP-29; CNP-
DE 53].
GN Name=Nppc; Synonyms=Cnp;
OS Rattus norvegicus (Rat).

```

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 CC Muridae; Muridae; Murinae; Rattus;
 CC NCBI_TaxID=10116;
 RN (1)
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE:9192420; PubMed:1702395; DOI=10.1016/0014-5793(90)80544-S;
 RA Kojima M., Miamano N., Kangawa K., Matsuo H.;
 RT "Cloning and sequence analysis of a cDNA encoding a precursor for rat
 C-type natriuretic peptide (CNP).";
 RL FEBS Lett. 276:209-213(1990).
 CC CC
 CC -1- FUNCTION: Vasorelaxant activity. Has a cGMP-stimulating activity.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed exclusively in brain.
 CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
 CC -----
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 CC -----
 CC EMBL: D90219; BAA14250.1; -; mRNA.
 DR PIR: S12988; S12988.
 DR Ensembl: ENSRNOG0000018854; Rattus norvegicus.
 DR RGD: 620850; Npdc.
 DR InterPro: IPR002406; C_natriurecep.
 DR InterPro: IPR000663; Natr_peptide.
 DR Pfam: PF00212; ANP; 1.
 DR PRINTS: PR00713; CNATPEPTIDE.
 DR PRINTS: PR00710; NATPEPTIDES.
 DR Prodom: PD005617; Natr_peptide; 1.
 DR SMART: SM00183; NAT_PEP; 1.
 DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
 KW Hormone; Signal; Vasocative.
 FT SIGNAL 1 23 Potential.
 FT PROPEP 24 72
 FT PEPTIDE 74 126 CNP-53.
 FT PEPTIDE 98 126 CNP-29 (By similarity).
 FT PEPTIDE 105 126 CNP-22.
 FT DISULFID 110 126 By similarity.
 SQ SEQUENCE 126 AA; 13314 MW; 0957A0DB58C82E08 CRC64;
 Query Match 80.9%; Score 55; DB 1; Length 126;
 Best Local Similarity 58.8%; Pred. No. 0.00086;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CFGXXXDRIGXXSXXGC 17
 DB 110 CFGKLDRIGSMGSLGC 126
 RESULT 45
 ANFC_SHEEP STANDARD; PRT; 126 AA.
 ID P56283.
 AC 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE C-type natriuretic peptide precursor [Contains: CNP-22; CNP-29; CNP-53].
 OS Name=NPPC; Synonym=CNP;
 OS Ovis aries (Sheep);
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 CC Pecora; Bovidae; Caprinae; Ovis.
 CC NCBI_TaxID=9940;
 RN (1)
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE:99236261; PubMed:10219521; DOI=10.1016/S0739-7240(99)00005-3;
 RA Aitken G.D., Ratis A.M., Yandle T.G., George P.M., Espiner E.A.,
 RA Cameron V.A.;
 RT "The characterization of ovine genes for atrial, brain, and C-type

RT natriuretic peptides.";
 RL Domest. Anim. Endocrinol. 16:115-121(1999).
 CC CC
 CC -1- FUNCTION: Vasorelaxant activity. Has a cGMP-stimulating activity.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
 CC -----
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 CC -----
 CC EMBL: AF037467; AAB92261.1; -; Genomic DNA.
 DR InterPro: IPR002406; C_natriurecep.
 DR InterPro: IPR000663; Natr_peptide.
 DR Pfam: PF00212; ANP; 1.
 DR PRINTS: PR00713; CNATPEPTIDE.
 DR PRINTS: PR00710; NATPEPTIDES.
 DR Prodom: PD005617; Natr_peptide; 1.
 DR SMART: SM00183; NAT_PEP; 1.
 DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
 KW Hormone; Signal; Vasocative.
 FT SIGNAL 1 23 Potential.
 FT PROPEP 24 72
 FT PEPTIDE 74 126 CNP-53 (By similarity).
 FT PEPTIDE 98 126 CNP-29 (By similarity).
 FT PEPTIDE 105 126 CNP-22.
 FT DISULFID 110 126 By similarity.
 SQ SEQUENCE 126 AA; 13317 MW; 83C21B3C49A8F18B CRC64;
 Query Match 80.9%; Score 55; DB 1; Length 126;
 Best Local Similarity 58.8%; Pred. No. 0.00086;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CFGXXXDRIGXXSXXGC 17
 DB 110 CFGKLDRIGSMGSLGC 126
 RESULT 46
 Q4ZG41 HUMAN PRELIMINARY; PRT; 126 AA.
 ID Q4ZG41.
 AC Q4ZG41.
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Hypothetical protein NPPC.
 GN Name=NPPC;
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 CC Homo.
 CC NCBI_TaxID=9606;
 RN (1)
 RN NUCLEOTIDE SEQUENCE.
 RP Kozlovicz A., Spalding L., Tomlinson C.;
 RT "The sequence of Homo sapiens BAC clone RP11-52C8.";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.H.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN (3)
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN (4)
 RN NUCLEOTIDE SEQUENCE.
 RA Wilson R.K.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC013435; AAX88912.1; -; Genomic DNA.
 DR InterPro: IPR002406; C_natriurecep.
 DR InterPro: IPR000663; Natr_peptide.

DR Pfam: PF00212; ANP; 1.
 DR PRINTS; PR00713; CNATPEPTIDE.
 DR PRINTS; PR00710; NATPEPTIDES.
 DR PRODOM; PD005617; Natr_peptide; 1.
 DR SMART; SM00183; NAT_PEP; 1.
 DR PROSITE; PS00263; NATRIURETIC PEPTIDE; 1.
 KW Hypothetical protein; Vasocactive.
 SQ SEQUENCE 126 AA; 13246 MW; 58F6E657866F9A2D CRC64;
 Query Match 80.9%; Score 55; DB 2; Length 126;
 Best Local Similarity 58.8%; Pred. No. 0.00086;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CFGXXXDRIGXXXGXC 17
 DB 110 CFGCLKDRIGSWGSLGC 126
 RESULT 47
 ID Q54K5_MOUSE PRELIMINARY; PRT; 126 AA.
 AC Q54K5;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE 16 days neonate cerebellum cDNA, RIKEN full-length enriched library,
 DE clone:9630044D15 product:natriuretic peptide type C, full insert
 DE sequence.
 GN Name=NpPC;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
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 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=9927923; PubMed=10349666; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi U., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuenl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Bash G.,
 RA Blake U., Boefelli D., Bojunga N., Carninci P., de Bonaldi M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guscinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima U., Mazzarelli I., Monbarts P.,
 RA Norioka P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Schenbach C., Seta T., Shibata Y., Schorch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=22354683; PubMed=1246851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi U., Bono H., Kondo S.,
 RA Nikaido I., Otsu N., Saito R., Suzuki H., Yamana K.I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schenbach C., Gojobori T.,
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Brad D., Brusio V., Chochia C., Cobanli L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gong J.,
 RA Grimmond S., Guscinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.,
 RA Kongawa A., Kurochkin I.V., Lee Y., Lemhar B., Lyons P.A.,
 RA Maglott D.R., Maltsev L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pereira G.,
 RA Petrovsky N., Pillai R., Pontius U.V., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandella A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wymshaw-Boris A., Yanagisawa M., Yang L., Yang L.,
 RA Yuan Z., Zavoian M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirokane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai U., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasuniishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/9r.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugihara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/9r.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama U., Nishi K., Katsunari T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai U.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RA Adachi U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirokawa T., Hirozane T.,
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai U., Kojima Y., Kondo S., Kono H., Konda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki K., Ono M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Saeki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takada Y., Tanaka T.,
 RA Tomaru A., Taya T., Yasuniishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBD databases.
 DR EMBL; AK036176; BAC29333.1; -, mRNA.
 DR MGI; MGI:97369; NpPC.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005184; F:neuropeptide hormone activity; TAS.
 DR GO; GO:0005102; F:receptor binding; IDA.
 DR GO; GO:0006182; P:cGMP biosynthesis; IDA.
 KW Vasocactive.
 SQ SEQUENCE 126 AA; 13320 MW; 8F55B1C4EB2F0ACB CRC64;
 Query Match 80.9%; Score 55; DB 2; Length 126;

Best Local Similarity 58.8%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXSXXGC 17
DB 110 CFGKLDRIGSWSGLGC 126

RESULT 48

ANFB_SHEEP STANDARD; PRT; 129 AA.
ID ANFB_SHEEP
AC 046541;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Natriuretic peptides B precursor (Contains: Gamma-brain natriuretic peptide; Brain natriuretic peptide 29 (BNP-29); Brain natriuretic peptide 26 (BNP-26)).
GN Name=NPBP;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=99236261; PubMed=10219521; DOI=10.1016/S0739-7240(99)00005-3;
RX Altken G.D., Raizis A.M., Yandle T.G., George P.M., Espiner E.A., Cameron V.A.;
RA "The characterization of ovine genes for atrial, brain, and C-type natriuretic peptides.";
RT Biochem. Biophys. Res. Commun. 16:115-121(1999).
RT Domest. Anim. Endocrinol. 16:115-121(1999).
CC -1- FUNCTION: Acts as a cardiac hormone with a variety of biological actions including natriuresis, diuresis, vasorelaxation, and inhibition of renin and aldosterone secretion. It is thought to play a key role in cardiovascular homeostasis. Helps restore the body's salt and water balance. Improves heart function.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.

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CC -----
CC EMBL; AF037466; AAB92565.1; -; Genomic DNA.
CC InterPro; IPR002408; Br_natriureticpep.
CC InterPro; IPR000663; Natri_peptide.
CC Pfam; PF00212; ANP; 1.
CC PRINTS; PR00712; BNATPEPTIDE.
CC PRINTS; PR00710; NATPEPTIDES.
CC PRODOM; PD005617; Natri_peptide; 1.
CC SMART; SM00183; NAT_PEP; 1.
CC PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
CC KW Hormone; Signal; Vasoactive.
CC SIGNAL 1 26 Potential.
CC CHAIN 27 129 Gamma-brain natriuretic peptide.
CC PEPTIDE 101 129 Brain natriuretic peptide 29 (By similarity).
CC PEPTIDE 104 129 Brain natriuretic peptide 26 (By similarity).
CC DISULFID 107 123 By similarity.
CC SEQUENCE 129 AA; 14118 MW; 1304DF91D32A28EF CRC64;

Query Match 80.9%; Score 55; DB 1; Length 129;
Best Local Similarity 58.8%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXSXXGC 17
DB 107 CFGRLDRIGSWSGLGC 123

RESULT 49

ANFC_RANCA STANDARD; PRT; 129 AA.
ID ANFC_RANCA
AC P20968;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide-1 precursor (CNP I).
OS Rana catesbeiana (Bull Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana; Agarana.
OC NCBI_TaxID=8400;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Brain;
RC TISSUE=Brain;
RX MEDLINE=94230409; PubMed=8175740;
RA Kojima M., Ohyama Y., Miyamoto K., Minamino N., Kangawa K., Matsuo H.;
RT "Cloning and characterization of a novel natriuretic peptide in frog (Rana catesbeiana)."
RT J. Biol. Chem. 269:13136-13140(1994).
RN [2]
RP PROTEIN SEQUENCE OF 108-129.
RC TISSUE=Brain;
RX MEDLINE=91083642; PubMed=2148082;
RA Yoshinaka A., Kozawa H., Minamino N., Kangawa K., Matsuo H.;
RT "Isolation and sequence determination of frog C-type natriuretic peptide.";
RT Biochem. Biophys. Res. Commun. 173:591-598(1990).
CC -1- FUNCTION: Exhibits natriuretic and vasodepressor activity. Has a GMP-stimulating activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.

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CC -----
CC EMBL; D17413; BAA04235.1; -; mRNA.
CC PIR; A36399; A36399.
CC PIR; A54119; A54119.
CC InterPro; IPR002406; C_natriureticpep.
CC InterPro; IPR000663; Natri_peptide.
CC Pfam; PF00212; ANP; 1.
CC PRINTS; PR00713; CNATPEPTIDE.
CC PRINTS; PR00710; NATPEPTIDES.
CC PRODOM; PD005617; Natri_peptide; 1.
CC SMART; SM00183; NAT_PEP; 1.
CC PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
CC KW Direct protein sequencing; Hormone; Signal; Vasoactive.
CC SIGNAL 1 24 Potential.
CC PROPEP 25 105 C-type natriuretic peptide-1.
CC PEPTIDE 108 129
CC DISULFID 113 129
CC SEQUENCE 129 AA; 14656 MW; 47E0E78E32F07307 CRC64;

Query Match 80.9%; Score 55; DB 1; Length 129;
Best Local Similarity 58.8%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXSXXGC 17
DB 113 CFGVLDRIIGAFSGGLGC 129

RESULT 50
ANFC2_FUGRU STANDARD; PRT; 130 AA.
ID ANFC2_FUGRU
AC Q805D5;
DT 25-OCT-2004 (Rel. 45, Created)

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DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE C-type natriuretic peptide-2 precursor.
GN Name=cnp-2;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX PubMed=12893874; DOI=10.1073/pnas.1633368100;
RA Inoue K., Naruse K., Yamagami S., Mitani H., Suzuki N., Takel Y.;
RT "Four functionally distinct C-type natriuretic peptides found in fish
RT reveal evolutionary history of the natriuretic peptide system.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:10079-10084(2003).
CC -!- FUNCTION: Exhibits natriuretic and vasodepressant activity. Has
CC GMP-stimulating activity. May help to regulate body fluid
CC homeostasis in a variety of aquatic environments.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the natriuretic peptide family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL, AB089936; BAC57072.1; -; mRNA.
DR Ensembl, SINFRUG00000157592; Fugu rubripes.
DR InterPro, IPR002406; C_natriureticp.
DR InterPro, IPR000663; Natr_peptide.
DR Pfam, PF00212; ANP; 1.
DR PRINTS; PR00713; CNATPEPTIDE.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
DR Hormone; Signal; Vasocactive.
FT SIGNAL 1 22 Potential.
FT PROPEP 23 101 By similarity.
FT PEPTIDE 104 130 C-type natriuretic peptide-2.
FT DISULFID 114 130 By similarity.
SQ SEQUENCE 130 AA; 13792 MW; 41BE1FC1A5F7E4C CRC64;

Query Match 80.9%; Score 55; DB 1; Length 130;
Best Local Similarity 58.8%; Pred. No. 0.00088;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Search completed: January 26, 2006, 14:45:17
 Job time : 91 secs

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OM protein - protein search, using sw model

Run on: January 26, 2006, 14:40:37 : Search time 23 Seconds
(without alignments)
61.108 Million cell updates/sec

Title: US-10-664-605-5
Perfect score: 68
Sequence: 1 CFGXXXDRIGXXSXGC 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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3: /cgn2_6/ptodata/1/1aa/H/COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	82.4	20	2	US-09-579-883A-13 Sequence 13, Appl
2	56	82.4	20	2	US-09-623-548A-469 Sequence 469, App
3	56	82.4	20	2	US-09-657-276-469 Sequence 469, App
4	56	82.4	21	2	US-09-623-548A-470 Sequence 470, App
5	56	82.4	21	2	US-09-657-276-470 Sequence 470, App
6	56	82.4	23	6	5212286-43 Patent No. 5212286
7	56	82.4	23	6	5212286-47 Patent No. 5212286
8	56	82.4	24	1	US-07-754-958-4 Sequence 4, Appli
9	56	82.4	24	1	US-07-754-947-4 Sequence 468, App
10	56	82.4	24	2	US-09-623-548A-468 Sequence 471, App
11	56	82.4	24	2	US-09-623-548A-471 Sequence 468, App
12	56	82.4	24	2	US-09-657-276-468 Sequence 471, App
13	56	82.4	24	2	US-09-657-276-471 Sequence 471, App
14	56	82.4	25	6	5212286-31 Patent No. 5212286
15	56	82.4	25	6	5212286-35 Patent No. 5212286
16	56	82.4	28	1	US-08-451-240-14 Sequence 14, Appl
17	56	82.4	28	1	US-08-470-846A-14 Sequence 14, Appl
18	56	82.4	28	1	US-09-154-390-14 Sequence 14, Appl
19	56	82.4	28	4	PCT-US94-12591-14 Sequence 14, Appl
20	56	82.4	30	2	US-09-623-548A-472 Sequence 472, App
21	56	82.4	30	2	US-09-657-276-472 Sequence 472, App
22	55	80.9	17	1	US-07-828-450-7 Sequence 7, Appli
23	55	80.9	17	1	US-08-737-927-1 Sequence 1, Appli
24	55	80.9	17	1	US-08-850-910A-15 Sequence 15, Appl
25	55	80.9	17	2	US-09-623-548A-474 Sequence 474, App
26	55	80.9	17	2	US-09-657-276-474 Sequence 474, App
27	55	80.9	17	2	US-09-902-517-15 Sequence 15, Appl

28	55	80.9	20	1	US-08-850-910A-32 Sequence 32, Appl
29	55	80.9	20	1	US-08-850-910A-34 Sequence 34, Appl
30	55	80.9	20	2	US-09-902-517-32 Sequence 32, Appl
31	55	80.9	20	2	US-09-902-517-34 Sequence 34, Appl
32	55	80.9	20	6	5212286-30 Patent No. 5212286
33	55	80.9	20	6	5212286-51 Patent No. 5212286
34	55	80.9	21	1	US-08-257-446-2 Sequence 2, Appli
35	55	80.9	21	2	US-09-623-548A-483 Sequence 483, App
36	55	80.9	21	2	US-09-657-276-483 Sequence 483, App
37	55	80.9	21	6	5212286-41 Patent No. 5212286
38	55	80.9	22	1	US-07-754-958-1 Sequence 1, Appli
39	55	80.9	22	1	US-07-754-958-7 Sequence 7, Appli
40	55	80.9	22	1	US-07-754-947-1 Sequence 1, Appli
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42	55	80.9	22	1	US-07-728-221B-2 Sequence 2, Appli
43	55	80.9	22	1	US-07-728-221B-11 Sequence 11, Appl
44	55	80.9	22	1	US-07-778-847-3 Sequence 3, Appli
45	55	80.9	22	1	US-07-828-450-2 Sequence 2, Appli
46	55	80.9	22	1	US-07-828-450-8 Sequence 8, Appli
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51	55	80.9	22	1	US-07-828-450-13 Sequence 13, Appl
52	55	80.9	22	1	US-07-828-450-14 Sequence 14, Appl
53	55	80.9	22	1	US-07-828-450-15 Sequence 15, Appl
54	55	80.9	22	1	US-07-828-450-16 Sequence 16, Appl
55	55	80.9	22	1	US-07-828-450-22 Sequence 22, Appl
56	55	80.9	22	1	US-07-828-450-23 Sequence 23, Appl
57	55	80.9	22	1	US-07-828-450-24 Sequence 24, Appl
58	55	80.9	22	1	US-07-828-450-25 Sequence 25, Appl
59	55	80.9	22	1	US-07-828-450-31 Sequence 31, Appl
60	55	80.9	22	1	US-07-828-450-42 Sequence 42, Appl
61	55	80.9	22	1	US-08-257-446-1 Sequence 1, Appli
62	55	80.9	22	1	US-08-297-330-3 Sequence 3, Appli
63	55	80.9	22	1	US-08-297-330-9 Sequence 9, Appli
64	55	80.9	22	1	US-08-451-240-4 Sequence 4, Appli
65	55	80.9	22	1	US-08-470-846A-4 Sequence 4, Appli
66	55	80.9	22	2	US-07-728-220C-21 Sequence 21, Appl
67	55	80.9	22	2	US-09-466-268B-9 Sequence 9, Appli
68	55	80.9	22	2	US-09-154-390-4 Sequence 4, Appli
69	55	80.9	22	2	US-10-106-806-8 Sequence 8, Appli
70	55	80.9	22	2	US-10-106-806-9 Sequence 9, Appli
71	55	80.9	22	2	US-09-623-548A-475 Sequence 475, App
72	55	80.9	22	2	US-09-623-548A-508 Sequence 508, App
73	55	80.9	22	2	US-09-623-548A-517 Sequence 517, App
74	55	80.9	22	2	US-09-623-548A-518 Sequence 518, App
75	55	80.9	22	2	US-09-657-276-475 Sequence 475, App
76	55	80.9	22	2	US-09-657-276-508 Sequence 508, App
77	55	80.9	22	2	US-09-657-276-517 Sequence 517, App
78	55	80.9	22	2	US-09-657-276-518 Sequence 518, App
79	55	80.9	22	4	PCT-US94-02391-3 Sequence 3, Appli
80	55	80.9	22	4	PCT-US94-02391-9 Sequence 9, Appli
81	55	80.9	22	4	PCT-US94-12591-4 Sequence 4, Appli
82	55	80.9	22	6	5212286-38 Patent No. 5212286
83	55	80.9	22	6	5212286-40 Patent No. 5212286
84	55	80.9	23	1	US-07-828-450-3 Sequence 3, Appli
85	55	80.9	23	1	US-07-828-450-6 Sequence 6, Appli
86	55	80.9	23	2	US-09-623-548A-481 Sequence 481, App
87	55	80.9	23	2	US-09-623-548A-484 Sequence 484, App
88	55	80.9	23	2	US-09-623-548A-524 Sequence 524, App
89	55	80.9	23	2	US-09-657-276-481 Sequence 481, App
90	55	80.9	23	2	US-09-657-276-484 Sequence 484, App
91	55	80.9	23	2	US-09-657-276-524 Sequence 524, App
92	55	80.9	23	6	5212286-29 Patent No. 5212286
93	55	80.9	23	6	5212286-37 Patent No. 5212286
94	55	80.9	23	6	5212286-39 Patent No. 5212286
95	55	80.9	23	6	5212286-50 Patent No. 5212286
96	55	80.9	24	1	US-08-257-446-5 Sequence 5, Appli
97	55	80.9	24	2	US-09-623-548A-473 Sequence 473, App
98	55	80.9	24	2	US-09-623-548A-485 Sequence 485, App
99	55	80.9	24	2	US-09-623-548A-487 Sequence 487, App
100	55	80.9	24	2	US-09-623-548A-502 Sequence 502, App

101	55	80.9	24	2	US-09-623-548A-505	Sequence 505, App	174	55	80.9	28	2	US-09-154-390-23	Sequence 23, Appl
102	55	80.9	24	2	US-09-657-276-473	Sequence 473, App	175	55	80.9	28	2	US-10-106-806-5	Sequence 5, Appl1
103	55	80.9	24	2	US-09-657-276-485	Sequence 485, App	176	55	80.9	28	2	US-09-623-548A-476	Sequence 476, App
104	55	80.9	24	2	US-09-657-276-487	Sequence 487, App	177	55	80.9	28	2	US-09-623-548A-486	Sequence 486, App
105	55	80.9	24	2	US-09-657-276-502	Sequence 502, App	178	55	80.9	28	2	US-09-623-548A-495	Sequence 495, App
106	55	80.9	24	2	US-09-657-276-505	Sequence 505, App	179	55	80.9	28	2	US-10-360-101-84	Sequence 84, Appl
107	55	80.9	24	6	5212286-26	Patent No. 5212286	180	55	80.9	28	2	US-09-657-276-476	Sequence 476, App
108	55	80.9	24	6	5212286-28	Patent No. 5212286	181	55	80.9	28	2	US-09-657-276-486	Sequence 486, App
109	55	80.9	25	1	US-08-850-910A-2	Sequence 2, Appl1	182	55	80.9	28	2	US-09-657-276-495	Sequence 495, App
110	55	80.9	25	2	US-09-623-548A-480	Sequence 480, App	183	55	80.9	28	4	PCT-US94-0231-1	Sequence 1, Appl1
111	55	80.9	25	2	US-09-623-548A-488	Sequence 488, App	184	55	80.9	28	4	PCT-US94-12591-9	Sequence 9, Appl1
112	55	80.9	25	2	US-09-657-276-480	Sequence 480, App	185	55	80.9	28	6	PCT-US94-12591-21	Sequence 21, Appl1
113	55	80.9	25	2	US-09-657-276-488	Sequence 488, App	186	55	80.9	28	6	5204327-1	Patent No. 5204327
114	55	80.9	25	2	US-09-902-517-2	Sequence 2, Appl1	187	55	80.9	28	6	5204327-3	Patent No. 5204327
115	55	80.9	25	6	5202239-16	Patent No. 5202239	188	55	80.9	28	6	5449751-2	Patent No. 5449751
116	55	80.9	25	6	5212286-25	Patent No. 5212286	189	55	80.9	28	6	5461142-1	Patent No. 5461142
117	55	80.9	25	6	5212286-27	Patent No. 5212286	190	55	80.9	29	1	US-07-754-947-6	Sequence 6, Appl1
118	55	80.9	25	6	5212286-34	Patent No. 5212286	191	55	80.9	29	1	US-08-448-219-5	Sequence 6, Appl1
119	55	80.9	26	1	US-07-778-847-2	Sequence 2, Appl1	192	55	80.9	29	1	US-09-623-548A-465	Sequence 465, App
120	55	80.9	26	1	US-08-850-910A-1	Sequence 1, Appl1	193	55	80.9	29	2	US-09-657-276-465	Sequence 465, App
121	55	80.9	26	1	US-09-623-548A-478	Sequence 3, Appl1	194	55	80.9	29	2	US-09-657-276-465	Sequence 465, App
122	55	80.9	26	2	US-09-623-548A-479	Sequence 478, App	195	55	80.9	31	2	US-09-026-216-22	Sequence 22, Appl
123	55	80.9	26	2	US-09-623-548A-479	Sequence 479, App	196	55	80.9	31	2	US-09-964-201A-82	Sequence 22, Appl
124	55	80.9	26	2	US-09-623-548A-511	Sequence 511, App	197	55	80.9	32	1	US-07-754-958-5	Sequence 5, Appl1
125	55	80.9	26	2	US-09-657-276-478	Sequence 478, App	198	55	80.9	32	1	US-07-754-947-5	Sequence 5, Appl1
126	55	80.9	26	2	US-09-657-276-479	Sequence 479, App	199	55	80.9	32	1	US-08-451-240-2	Sequence 2, Appl1
127	55	80.9	26	2	US-09-657-276-511	Sequence 511, App	200	55	80.9	32	1	US-08-737-927-4	Sequence 4, Appl1
128	55	80.9	26	2	US-09-902-517-3	Sequence 3, Appl1	201	55	80.9	32	1	US-08-470-846A-18	Sequence 18, Appl
129	55	80.9	27	1	US-07-828-450-4	Sequence 4, Appl1	202	55	80.9	32	2	US-08-954-915A-44	Sequence 44, Appl
130	55	80.9	27	1	US-07-828-450-5	Sequence 5, Appl1	203	55	80.9	32	2	US-08-954-915A-45	Sequence 45, Appl
131	55	80.9	27	1	US-08-297-330-4	Sequence 4, Appl1	204	55	80.9	32	2	US-09-068-738A-2	Sequence 2, Appl1
132	55	80.9	27	2	US-09-623-548A-482	Sequence 482, App	205	55	80.9	32	2	US-09-068-738A-17	Sequence 17, Appl
133	55	80.9	27	2	US-09-623-548A-491	Sequence 491, App	206	55	80.9	32	2	US-09-154-390-2	Sequence 2, Appl1
134	55	80.9	27	2	US-09-623-548A-501	Sequence 501, App	207	55	80.9	32	2	US-09-623-548A-490	Sequence 490, App
135	55	80.9	27	2	US-09-623-548A-523	Sequence 523, App	208	55	80.9	32	2	US-09-623-548A-504	Sequence 504, App
136	55	80.9	27	2	US-10-360-101-25	Sequence 25, App	209	55	80.9	32	2	US-09-623-548A-507	Sequence 507, App
137	55	80.9	27	2	US-10-360-101-88	Sequence 88, Appl	210	55	80.9	32	2	US-09-623-548A-512	Sequence 512, App
138	55	80.9	27	2	US-09-657-276-482	Sequence 482, App	211	55	80.9	32	2	US-09-623-548A-513	Sequence 513, App
139	55	80.9	27	2	US-09-657-276-491	Sequence 491, App	212	55	80.9	32	2	US-09-657-276-480	Sequence 490, App
140	55	80.9	27	2	US-09-657-276-501	Sequence 501, App	213	55	80.9	32	2	US-09-657-276-504	Sequence 504, App
141	55	80.9	27	2	US-09-657-276-523	Sequence 523, App	214	55	80.9	32	2	US-09-657-276-507	Sequence 507, App
142	55	80.9	27	4	PCT-US94-02391-4	Sequence 523, App	215	55	80.9	32	2	US-09-657-276-512	Sequence 512, App
143	55	80.9	27	6	5202239-5	Patent No. 5202239	216	55	80.9	32	2	US-09-657-276-513	Sequence 513, App
144	55	80.9	28	1	US-07-754-958-2	Sequence 2, Appl1	217	55	80.9	32	4	PCT-US94-12591-2	Sequence 2, Appl1
145	55	80.9	28	1	US-07-754-958-3	Sequence 3, Appl1	218	55	80.9	32	6	5449751-1	Patent No. 5449751
146	55	80.9	28	1	US-07-754-947-2	Sequence 2, Appl1	219	55	80.9	32	6	5449751-3	Patent No. 5449751
147	55	80.9	28	1	US-07-754-947-3	Sequence 3, Appl1	220	55	80.9	37	2	US-09-466-268B-2	Sequence 2, Appl1
148	55	80.9	28	1	US-07-778-847-1	Sequence 1, Appl1	221	55	80.9	37	2	US-10-106-806-2	Sequence 2, Appl1
149	55	80.9	28	1	US-07-781-590A-12	Sequence 12, Appl	222	55	80.9	45	1	US-09-902-517-50	Sequence 50, Appl
150	55	80.9	28	1	US-07-781-590A-13	Sequence 13, Appl	223	55	80.9	45	1	US-07-757-606B-4	Sequence 4, Appl1
151	55	80.9	28	1	US-07-781-590A-14	Sequence 14, Appl	224	55	80.9	45	2	US-08-954-915A-46	Sequence 46, Appl
152	55	80.9	28	1	US-07-828-450-1	Sequence 1, Appl1	225	55	80.9	45	2	US-08-954-915A-47	Sequence 47, Appl
153	55	80.9	28	1	US-07-828-450-17	Sequence 17, Appl	226	55	80.9	45	2	US-09-623-548A-510	Sequence 510, App
154	55	80.9	28	1	US-07-828-450-40	Sequence 40, Appl	227	55	80.9	45	2	US-09-623-548A-514	Sequence 514, App
155	55	80.9	28	1	US-08-184-935-3	Sequence 3, Appl1	228	55	80.9	45	2	US-09-657-276-510	Sequence 510, App
156	55	80.9	28	1	US-08-066-156-2	Sequence 2, Appl1	229	55	80.9	45	2	US-09-657-276-514	Sequence 514, App
157	55	80.9	28	1	US-08-297-330-1	Sequence 1, Appl1	230	55	80.9	53	1	US-07-728-221B-1	Sequence 1, Appl1
158	55	80.9	28	1	US-08-288-681A-2	Sequence 2, Appl1	231	55	80.9	53	1	US-07-728-221B-10	Sequence 10, Appl
159	55	80.9	28	1	US-08-451-240-9	Sequence 9, Appl1	232	55	80.9	53	2	US-07-728-220C-22	Sequence 22, Appl
160	55	80.9	28	1	US-08-451-240-21	Sequence 21, Appl	233	55	80.9	53	2	US-07-765-830A-2	Sequence 2, Appl1
161	55	80.9	28	1	US-08-240-711-21	Sequence 21, Appl	234	55	80.9	53	2	US-09-623-548A-519	Sequence 519, App
162	55	80.9	28	1	US-08-741-678-2	Sequence 2, Appl1	235	55	80.9	53	2	US-09-623-548A-520	Sequence 520, App
163	55	80.9	28	1	US-08-457-753-21	Sequence 21, Appl	236	55	80.9	53	2	US-10-360-101-87	Sequence 87, Appl
164	55	80.9	28	1	US-08-470-846A-2	Sequence 2, Appl1	237	55	80.9	53	2	US-09-657-276-519	Sequence 519, App
165	55	80.9	28	1	US-08-470-846A-9	Sequence 9, Appl1	238	55	80.9	53	2	US-09-657-276-520	Sequence 520, App
166	55	80.9	28	1	US-08-460-890A-53	Sequence 53, Appl1	239	55	80.9	56	2	US-09-623-548A-489	Sequence 489, App
167	55	80.9	28	2	US-08-954-915A-51	Sequence 51, Appl	240	55	80.9	56	2	US-09-657-276-489	Sequence 489, App
168	55	80.9	28	2	US-08-167-641C-53	Sequence 53, Appl	241	55	80.9	106	1	US-08-850-910A-30	Sequence 30, Appl
169	55	80.9	28	2	US-08-160-971A-53	Sequence 53, Appl	242	55	80.9	106	2	US-09-902-517-30	Sequence 30, Appl
170	55	80.9	28	2	US-08-462-040-53	Sequence 53, Appl	243	55	80.9	125	1	US-08-862-480B-1	Sequence 1, Appl1
171	55	80.9	28	2	US-09-466-268B-5	Sequence 53, Appl1	244	55	80.9	126	1	US-07-757-606B-1	Sequence 1, Appl1
172	55	80.9	28	2	US-09-154-390-9	Sequence 9, Appl1	245	55	80.9	126	1	US-07-757-606B-6	Sequence 6, Appl1
173	55	80.9	28	2	US-09-154-390-21	Sequence 21, Appl	246	55	80.9	126	2	US-07-728-220C-20	Sequence 20, Appl

247	55	80.9	126	2	US-07-765-830A-1	Sequence 1, Appl	320	49	72.1	25	6	5212286-55	Patent No. 5212286
248	55	80.9	126	2	US-07-765-830A-6	Sequence 6, Appl	321	48	70.6	17	1	US-08-850-910A-5	Sequence 5, Appl
249	55	80.9	126	2	US-07-765-830A-7	Sequence 7, Appl	322	48	70.6	17	2	US-09-902-517-5	Sequence 5, Appl
250	55	80.9	126	2	US-09-949-016-10041	Sequence 10041, A	323	48	70.6	22	1	US-07-828-450-18	Sequence 18, Appl
251	55	80.9	131	1	US-08-850-910A-39	Sequence 39, Appl	324	48	70.6	22	1	US-07-828-450-26	Sequence 26, Appl
252	55	80.9	131	1	US-08-850-910A-41	Sequence 41, Appl	325	48	70.6	22	1	US-07-828-450-27	Sequence 27, Appl
253	55	80.9	131	1	US-08-850-910A-43	Sequence 43, Appl	326	48	70.6	22	1	US-07-828-450-28	Sequence 28, Appl
254	55	80.9	131	1	US-08-850-910A-46	Sequence 46, Appl	327	48	70.6	22	1	US-07-828-450-29	Sequence 29, Appl
255	55	80.9	131	2	US-09-902-517-39	Sequence 39, Appl	328	48	70.6	23	1	US-07-781-590A-16	Sequence 16, Appl
256	55	80.9	131	2	US-09-902-517-41	Sequence 41, Appl	329	48	70.6	23	2	US-10-106-806-11	Sequence 11, Appl
257	55	80.9	131	2	US-09-902-517-43	Sequence 43, Appl	330	48	70.6	28	1	US-08-451-240-8	Sequence 8, Appl
258	55	80.9	131	2	US-09-902-517-46	Sequence 46, Appl	331	48	70.6	28	1	US-08-470-846A-8	Sequence 8, Appl
259	55	80.9	132	1	US-08-850-910A-47	Sequence 47, Appl	332	48	70.6	28	1	US-08-470-846A-22	Sequence 22, Appl
260	55	80.9	132	2	US-09-902-517-47	Sequence 47, Appl	333	48	70.6	28	2	US-09-154-390-8	Sequence 8, Appl
261	55	80.9	136	6	5212286-4	Patent No. 5212286	334	48	70.6	28	2	PCT-US94-12591-8	Sequence 8, Appl
262	55	80.9	144	6	5202239-1	Patent No. 5202239	335	48	70.6	32	2	US-08-954-915A-9	Sequence 9, Appl
263	55	80.9	144	6	5202239-3	Patent No. 5202239	336	48	70.6	33	2	US-09-623-548A-515	Sequence 515, App
264	55	80.9	151	2	US-08-916-043-5	Sequence 5, Appl	337	48	70.6	33	2	US-09-657-276-515	Sequence 515, App
265	55	80.9	151	2	US-09-428-929-5	Sequence 5, Appl	338	48	70.6	38	2	US-09-466-268B-10	Sequence 10, Appl
266	55	80.9	151	6	5212286-2	Patent No. 5212286	339	48	70.6	38	2	US-10-106-806-10	Sequence 10, Appl
267	55	80.9	152	2	US-08-916-043-2	Sequence 2, Appl	340	47	69.1	27	1	US-07-828-450-30	Sequence 30, Appl
268	55	80.9	152	2	US-09-428-929-2	Sequence 2, Appl	341	47	69.1	28	1	US-08-451-240-6	Sequence 6, Appl
269	55	80.9	152	6	5212286-6	Patent No. 5212286	342	47	69.1	28	1	US-08-470-846A-6	Sequence 6, Appl
270	55	80.9	241	6	5223425-11	Patent No. 5223425	343	47	69.1	28	1	US-08-470-846A-24	Sequence 24, Appl
271	54	79.4	23	6	5212286-48	Patent No. 5212286	344	47	69.1	28	2	US-08-954-915A-52	Sequence 52, Appl
272	54	79.4	25	6	5212286-36	Patent No. 5212286	345	47	69.1	28	2	US-09-154-390-6	Sequence 6, Appl
273	52	76.5	18	6	5212286-42	Patent No. 5212286	346	47	69.1	28	4	US-09-154-390-24	Sequence 24, Appl
274	51	75.0	32	2	US-08-954-915A-17	Sequence 17, Appl	347	47	69.1	28	4	PCT-US94-12591-6	Sequence 6, Appl
275	50	72.5	26	1	US-08-850-910A-1	Sequence 1, Appl	348	47	69.1	32	1	US-08-451-240-5	Sequence 5, Appl
276	50	72.5	26	2	US-10-106-806-7	Sequence 7, Appl	349	47	69.1	32	1	US-08-470-846A-5	Sequence 5, Appl
277	50	72.5	26	2	US-09-902-517-1	Sequence 1, Appl	350	47	69.1	32	2	US-09-154-390-5	Sequence 5, Appl
278	50	72.5	32	1	US-07-828-450-41	Sequence 41, Appl	351	47	69.1	32	4	PCT-US94-12591-5	Sequence 5, Appl
279	50	72.5	32	1	US-08-297-330-2	Sequence 2, Appl	352	46	67.6	17	1	US-07-828-450-19	Sequence 19, Appl
280	50	72.5	32	1	US-08-451-240-3	Sequence 3, Appl	353	46	67.6	21	1	US-07-781-590A-15	Sequence 15, Appl
281	50	72.5	32	1	US-08-451-240-22	Sequence 22, Appl	354	46	67.6	21	2	US-09-466-268B-8	Sequence 8, Appl
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283	50	72.5	32	2	US-08-954-915A-21	Sequence 21, Appl	356	46	67.6	28	1	US-08-470-846A-27	Sequence 27, Appl
284	50	72.5	32	2	US-08-954-915A-23	Sequence 23, Appl	357	46	67.6	28	2	US-08-954-915A-50	Sequence 50, Appl
285	50	72.5	32	2	US-08-954-915A-48	Sequence 48, Appl	358	46	67.6	28	2	US-09-154-390-27	Sequence 27, Appl
286	50	72.5	32	2	US-08-942-332B-1	Sequence 1, Appl	359	46	67.6	28	4	PCT-US94-12591-25	Sequence 25, Appl
287	50	72.5	32	2	US-08-942-456-1	Sequence 1, Appl	360	46	67.6	32	2	US-08-954-915A-1	Sequence 1, Appl
288	50	72.5	32	2	US-09-510-721-1	Sequence 1, Appl	361	45	66.2	27	6	5204327-2	Patent No. 5204327
289	50	72.5	32	2	US-09-466-268B-6	Sequence 6, Appl	362	45	66.2	20	1	US-08-257-446-3	Sequence 3, Appl
290	50	72.5	32	2	US-09-154-390-3	Sequence 3, Appl	363	44	64.7	32	2	US-08-954-915A-4	Sequence 4, Appl
291	50	72.5	32	2	US-09-154-390-22	Sequence 22, Appl	364	44	64.7	32	2	US-08-954-915A-11	Sequence 11, Appl
292	50	72.5	32	2	US-10-106-806-6	Sequence 6, Appl	365	44	64.7	32	2	US-08-954-915A-12	Sequence 12, Appl
293	50	72.5	32	2	US-09-623-548A-509	Sequence 509, App	366	44	64.7	32	2	US-08-954-915A-14	Sequence 14, Appl
294	50	72.5	32	2	US-09-623-548A-516	Sequence 516, App	367	44	64.7	32	2	US-08-954-915A-23	Sequence 23, Appl
295	50	72.5	32	2	US-09-657-276-509	Sequence 509, App	368	44	64.7	32	2	US-08-954-915A-43	Sequence 43, Appl
296	50	72.5	32	2	US-09-657-276-516	Sequence 516, App	369	43	63.2	32	2	US-08-954-915A-5	Sequence 5, Appl
297	50	72.5	32	2	US-09-902-517-49	Sequence 49, Appl	370	43	63.2	32	2	US-08-954-915A-15	Sequence 15, Appl
298	50	72.5	32	2	PCT-US94-02391-2	Sequence 2, Appl	371	43	63.2	32	2	US-08-954-915A-16	Sequence 16, Appl
299	50	72.5	32	4	PCT-US94-12591-3	Sequence 3, Appl	372	43	63.2	32	2	US-08-954-915A-19	Sequence 19, Appl
300	50	72.5	32	4	PCT-US94-12591-22	Sequence 22, Appl	373	43	63.2	32	2	US-08-954-915A-22	Sequence 22, Appl
301	50	72.5	33	2	US-09-942-709-1	Sequence 1, Appl	374	42	61.8	32	2	US-08-954-915A-6	Sequence 6, Appl
302	50	72.5	35	2	US-09-623-548A-506	Sequence 506, App	375	42	61.8	32	2	US-08-954-915A-13	Sequence 13, Appl
303	50	72.5	35	2	US-09-657-276-506	Sequence 506, App	376	42	61.8	32	2	US-08-954-915A-18	Sequence 18, Appl
304	50	72.5	41	2	US-10-106-806-1	Sequence 1, Appl	377	42	61.8	32	2	US-08-954-915A-26	Sequence 26, Appl
305	50	72.5	41	2	US-09-466-268B-1	Sequence 1, Appl	378	41	60.3	25	2	US-09-466-268B-7	Sequence 7, Appl
306	50	72.5	134	1	US-08-850-910A-45	Sequence 45, Appl	379	41	60.3	28	1	US-08-451-240-10	Sequence 10, Appl
307	50	72.5	134	1	US-08-850-910A-48	Sequence 48, Appl	380	41	60.3	28	1	US-08-470-846A-10	Sequence 10, Appl
308	50	72.5	134	2	US-09-508-435A-2	Sequence 2, Appl	381	41	60.3	28	2	US-09-154-390-10	Sequence 10, Appl
309	50	72.5	134	2	US-09-902-517-45	Sequence 45, Appl	382	41	60.3	28	4	PCT-US94-12591-10	Sequence 10, Appl
310	50	72.5	134	2	US-09-902-517-48	Sequence 48, Appl	383	41	60.3	32	2	US-10-360-101-86	Sequence 86, Appl
311	49	72.1	20	6	5212286-54	Patent No. 5212286	384	40	58.8	17	1	US-07-828-450-20	Sequence 20, Appl
312	49	72.1	20	6	5212286-58	Patent No. 5212286	385	40	58.8	17	1	US-08-257-446-4	Sequence 4, Appl
313	49	72.1	23	6	5212286-44	Patent No. 5212286	386	40	58.8	21	2	US-09-623-548A-196	Sequence 496, App
314	49	72.1	23	6	5212286-45	Patent No. 5212286	387	40	58.8	21	2	US-09-657-276-496	Sequence 496, App
315	49	72.1	23	6	5212286-53	Patent No. 5212286	388	40	58.8	22	1	US-07-781-590A-17	Sequence 17, Appl
316	49	72.1	24	6	5212286-52	Patent No. 5212286	389	40	58.8	25	6	5212286-49	Sequence 11, Appl
317	49	72.1	24	6	5212286-56	Patent No. 5212286	390	40	58.8	28	1	US-08-451-240-11	Sequence 23, Appl
318	49	72.1	25	6	5212286-32	Patent No. 5212286	391	40	58.8	28	1	US-08-451-240-23	Sequence 23, Appl
319	49	72.1	25	6	5212286-33	Patent No. 5212286	392	40	58.8	28	1	US-08-451-240-34	Sequence 34, Appl

393	40	58.8	28	1	US-08-470-846A-11	Sequence 11, Appl	466	33	48.5	28	2	US-09-154-390-39	Sequence 39, Appl
394	40	58.8	28	1	US-08-470-846A-19	Sequence 19, Appl	467	33	48.5	28	2	US-09-154-390-40	Sequence 40, Appl
395	40	58.8	28	1	US-08-470-846A-25	Sequence 25, Appl	468	33	48.5	28	4	PCT-US94-12591-16	Sequence 16, Appl
396	40	58.8	28	1	US-08-470-846A-31	Sequence 31, Appl	469	33	48.5	28	4	PCT-US94-12591-32	Sequence 32, Appl
397	40	58.8	28	1	US-08-470-846A-32	Sequence 32, Appl	470	33	48.5	28	4	PCT-US94-12591-35	Sequence 35, Appl
398	40	58.8	28	2	US-09-154-390-11	Sequence 11, Appl	471	33	48.5	32	2	US-08-954-915A-10	Sequence 10, Appl
399	40	58.8	28	2	US-09-154-390-19	Sequence 19, Appl	472	33	48.5	45	1	US-07-728-221B-9	Sequence 9, Appl
400	40	58.8	28	2	US-09-154-390-25	Sequence 25, Appl	473	33	47.1	22	1	US-08-451-240-29	Sequence 29, Appl
401	40	58.8	28	2	US-09-154-390-38	Sequence 38, Appl	474	32	47.1	22	1	US-08-451-240-30	Sequence 30, Appl
402	40	58.8	28	4	PCT-US94-12591-11	Sequence 11, Appl	475	32	47.1	22	1	US-08-470-846A-21	Sequence 21, Appl
403	40	58.8	28	4	PCT-US94-12591-23	Sequence 23, Appl	476	32	47.1	22	2	US-09-154-390-31	Sequence 31, Appl
404	40	58.8	28	4	PCT-US94-12591-34	Sequence 34, Appl	477	32	47.1	22	2	US-09-154-390-32	Sequence 32, Appl
405	40	58.8	32	1	US-08-451-240-15	Sequence 15, Appl	478	32	47.1	22	4	PCT-US94-12591-29	Sequence 29, Appl
406	40	58.8	32	1	US-08-470-846A-15	Sequence 15, Appl	479	32	47.1	22	4	PCT-US94-12591-30	Sequence 30, Appl
407	40	58.8	32	2	US-08-954-915A-20	Sequence 20, Appl	480	32	47.1	211	2	US-09-252-991A-18012	Sequence 18012, A
408	40	58.8	32	2	US-09-154-390-15	Sequence 15, Appl	481	32	47.1	301	2	US-09-252-991A-18062	Sequence 18062, A
409	40	58.8	32	2	PCT-US94-12591-15	Sequence 15, Appl	482	32	47.1	463	2	US-09-489-039A-8259	Sequence 8259, Ap
410	39.5	58.1	22	6	5212286-57	Patent No. 5212286	483	32	47.1	516	2	US-09-252-991A-21329	Sequence 21329, A
411	39	57.4	10	6	5212286-7	Patent No. 5212286	484	32	47.1	577	2	US-09-489-039A-9575	Sequence 9575, Ap
412	39	57.4	13	6	5212286-46	Patent No. 5212286	485	31	45.6	22	1	US-08-451-240-20	Sequence 20, Appl
413	39	57.4	15	2	US-09-623-548A-493	Sequence 493, App	486	31	45.6	22	1	US-08-470-846A-20	Sequence 20, Appl
414	39	57.4	15	2	US-09-657-276-493	Sequence 493, App	487	31	45.6	22	2	US-09-154-390-20	Sequence 20, Appl
415	39	57.4	22	2	US-09-466-268B-11	Sequence 11, Appl	488	31	45.6	22	4	PCT-US94-12591-20	Sequence 20, Appl
416	39	57.4	28	1	US-08-451-240-12	Sequence 12, Appl	489	31	45.6	28	1	US-08-451-240-17	Sequence 17, Appl
417	39	57.4	28	1	US-08-451-240-13	Sequence 13, Appl	490	31	45.6	28	1	US-08-451-240-31	Sequence 31, Appl
418	39	57.4	28	1	US-08-451-240-24	Sequence 24, Appl	491	31	45.6	28	1	US-08-470-846A-17	Sequence 17, Appl
419	39	57.4	28	1	US-08-470-846A-12	Sequence 12, Appl	492	31	45.6	28	2	US-09-154-390-17	Sequence 17, Appl
420	39	57.4	28	1	US-08-470-846A-13	Sequence 13, Appl	493	31	45.6	28	2	US-09-154-390-33	Sequence 33, Appl
421	39	57.4	28	1	US-08-470-846A-26	Sequence 26, Appl	494	31	45.6	28	4	PCT-US94-12591-17	Sequence 17, Appl
422	39	57.4	28	2	US-09-154-390-12	Sequence 12, Appl	495	31	45.6	28	4	PCT-US94-12591-31	Sequence 31, Appl
423	39	57.4	28	2	US-09-154-390-13	Sequence 13, Appl	496	31	45.6	29	1	US-08-451-240-27	Sequence 27, Appl
424	39	57.4	28	2	US-09-154-390-26	Sequence 26, Appl	497	31	45.6	29	1	US-08-451-240-28	Sequence 28, Appl
425	39	57.4	28	2	PCT-US94-12591-12	Sequence 12, Appl	498	31	45.6	29	1	US-08-470-846A-29	Sequence 29, Appl
426	39	57.4	28	4	PCT-US94-12591-13	Sequence 13, Appl	499	31	45.6	29	2	US-09-154-390-29	Sequence 29, Appl
427	39	57.4	28	4	PCT-US94-12591-24	Sequence 24, Appl	500	31	45.6	29	2	US-09-154-390-30	Sequence 30, Appl
428	39	57.4	32	2	US-08-954-915A-25	Sequence 25, Appl	501	31	45.6	29	4	PCT-US94-12591-27	Sequence 27, Appl
429	39	57.4	32	2	US-09-252-991A-30658	Sequence 30658, A	502	31	45.6	29	4	PCT-US94-12591-28	Sequence 28, Appl
430	38	55.9	28	1	US-08-470-846A-23	Sequence 23, Appl	503	31	45.6	263	2	US-09-489-039A-12011	Sequence 12011, A
431	38	55.9	32	2	US-08-954-915A-27	Sequence 27, Appl	504	31	45.6	417	2	US-09-489-039A-12036	Sequence 12036, A
432	38	55.9	32	2	US-08-954-915A-29	Sequence 29, Appl	505	31	45.6	449	2	US-09-489-039A-11553	Sequence 11553, A
433	37	54.4	15	6	5212286-24	Patent No. 5212286	506	31	45.6	480	2	US-09-489-039A-13045	Sequence 13045, A
434	37	54.4	21	2	US-09-623-548A-494	Sequence 494, App	507	31	45.6	569	2	US-09-252-991A-29263	Sequence 29263, A
435	37	54.4	21	2	US-09-657-276-494	Sequence 494, App	508	31	45.6	1666	2	US-09-948-016-8322	Sequence 8322, Ap
436	37	54.4	22	1	US-07-828-450-21	Sequence 21, Appl	509	30	44.1	12	2	US-09-349-707-8	Sequence 8, Appl
437	37	54.4	23	1	US-07-781-590A-2	Sequence 2, Appl	510	30	44.1	12	2	US-09-349-707-8	Sequence 8, Appl
438	37	54.4	23	1	US-07-781-590A-6	Sequence 6, Appl	511	30	44.1	19	1	US-07-828-450-32	Sequence 32, Appl
439	37	54.4	23	1	US-07-781-590A-10	Sequence 10, Appl	512	30	44.1	12	2	US-09-270-767-53701	Sequence 37501, A
440	37	54.4	23	1	US-07-781-590A-11	Sequence 11, Appl	513	30	44.1	138	2	US-09-270-767-53718	Sequence 52718, A
441	37	54.4	32	2	US-08-954-915A-2	Sequence 2, Appl	514	30	44.1	138	2	US-09-252-991A-21985	Sequence 21985, A
442	37	54.4	32	2	US-08-954-915A-3	Sequence 3, Appl	515	30	44.1	153	2	US-09-902-540-11201	Sequence 11201, A
443	37	54.4	32	2	US-08-954-915A-28	Sequence 28, Appl	516	30	44.1	153	2	US-09-902-540-11201	Sequence 11201, A
444	36	52.9	274	2	US-09-452-991A-23172	Sequence 23172, A	517	30	44.1	177	2	US-09-252-991A-29848	Sequence 29848, A
445	35	51.5	32	2	US-08-954-915A-8	Sequence 8, Appl	518	30	44.1	181	2	US-08-928-069-1	Sequence 1, Appl
446	35	51.5	32	2	US-08-954-915A-7	Sequence 7, Appl	519	30	44.1	181	2	US-08-928-069-1	Sequence 1, Appl
447	34	50.0	28	1	US-08-451-240-26	Sequence 26, Appl	520	30	44.1	255	2	US-09-949-016-8309	Sequence 8309, Ap
448	34	50.0	28	1	US-08-451-240-37	Sequence 37, Appl	521	30	44.1	294	2	US-09-270-767-59588	Sequence 59588, A
449	34	50.0	28	1	US-08-470-846A-28	Sequence 28, Appl	522	30	44.1	392	2	US-09-902-540-13511	Sequence 13511, A
450	34	50.0	28	2	US-08-470-846A-38	Sequence 38, Appl	523	30	44.1	405	2	US-09-489-039A-10525	Sequence 10525, A
451	34	50.0	28	2	US-09-154-390-28	Sequence 28, Appl	524	30	44.1	405	2	US-09-543-681A-3311	Sequence 4311, Ap
452	34	50.0	28	2	US-09-154-390-41	Sequence 41, Appl	525	30	44.1	411	2	US-09-902-540-15301	Sequence 15301, A
453	34	50.0	28	4	PCT-US94-12591-26	Sequence 26, Appl	526	30	44.1	415	2	US-09-134-000C-4092	Sequence 4092, Ap
454	34	50.0	28	4	PCT-US94-12591-36	Sequence 36, Appl	527	30	44.1	417	2	US-08-815-469-4	Sequence 4, Appl
455	34	50.0	28	4	PCT-US94-12591-37	Sequence 37, Appl	528	30	44.1	417	2	US-09-153-927-2	Sequence 2, Appl
456	34	50.0	32	2	US-08-954-915A-9	Sequence 9, Appl	529	30	44.1	417	2	US-09-566-918-5	Sequence 5, Appl
457	34	50.0	441	2	US-09-328-352-7754	Sequence 7754, Ap	530	30	44.1	417	2	US-08-928-069-10	Sequence 10, Appl
458	33	48.5	22	1	US-08-451-240-16	Sequence 16, Appl	531	30	44.1	417	2	US-08-828-683A-6	Sequence 6, Appl
459	33	48.5	28	1	US-08-451-240-32	Sequence 32, Appl	532	30	44.1	417	2	US-09-557-908-4	Sequence 4, Appl
460	33	48.5	28	1	US-08-451-240-33	Sequence 33, Appl	533	30	44.1	417	2	US-09-874-1308-5	Sequence 5, Appl
461	33	48.5	28	1	US-08-451-240-35	Sequence 35, Appl	534	30	44.1	417	2	US-09-333-966-4	Sequence 4, Appl
462	33	48.5	28	1	US-08-451-240-36	Sequence 36, Appl	535	30	44.1	417	2	US-09-565-009B-5	Sequence 5, Appl
463	33	48.5	28	1	US-08-470-846A-16	Sequence 16, Appl	536	30	44.1	417	2	US-10-175-902-5	Sequence 5, Appl
464	33	48.5	28	2	US-09-154-390-16	Sequence 16, Appl	537	30	44.1	417	2	US-09-314-889-4	Sequence 4, Appl
465	33	48.5	28	2	US-09-154-390-34	Sequence 34, Appl	538	30	44.1	420	2	US-09-252-991A-27610	Sequence 27610, A

539	30	44.1	428	2	US-08-815-469-2	612	28	41.2	77	2	US-09-248-796A-25522	Sequence 25522, A
540	30	44.1	428	2	US-09-557-908-2	613	28	41.2	90	1	US-08-308-086-6	Sequence 6, Appl1
541	30	44.1	428	2	US-09-333-966-2	614	28	41.2	92	1	US-08-446-038B-21	Sequence 21, Appl1
542	30	44.1	428	2	US-09-314-889-2	615	28	41.2	92	1	US-08-446-010B-21	Sequence 21, Appl1
543	30	44.1	430	2	US-09-252-991A-22599	616	28	41.2	92	1	US-08-479-078-11	Sequence 18, Appl1
544	30	44.1	444	2	US-09-328-352-5249	617	28	41.2	92	1	US-08-805-445-21	Sequence 21, Appl1
545	30	44.1	446	2	US-09-949-016-7652	618	28	41.2	92	1	US-08-064-067D-21	Sequence 21, Appl1
546	30	44.1	474	2	US-09-489-039A-6680	619	28	41.2	92	1	US-09-066-208-21	Sequence 21, Appl1
547	30	44.1	513	2	US-09-252-991A-22040	620	28	41.2	94	1	US-09-167-035-23	Sequence 23, Appl1
548	30	44.1	565	2	US-09-252-991A-28203	621	28	41.2	94	1	US-08-108-887A-23	Sequence 23, Appl1
549	30	44.1	585	2	US-09-248-796A-20176	622	28	41.2	94	1	US-08-538-086-23	Sequence 23, Appl1
550	30	44.1	833	2	US-09-013-895A-5	623	28	41.2	94	1	US-09-280-598-25	Sequence 25, Appl1
551	30	44.1	833	2	US-09-448-868-5	624	28	41.2	99	2	US-09-902-540-10041	Sequence 10041, A
552	30	44.1	833	2	US-10-226-296-5	625	28	41.2	124	2	US-09-489-039A-13811	Sequence 13811, A
553	30	44.1	833	2	US-09-252-991A-33134	626	28	41.2	124	2	US-09-902-540-10838	Sequence 10838, A
554	30	44.1	1140	2	US-09-651-656-21	627	28	41.2	140	2	US-09-489-039A-12841	Sequence 12841, A
555	30	44.1	1140	2	US-09-650-855-21	628	28	41.2	141	2	US-09-543-661A-4923	Sequence 4923, Ap
556	30	44.1	2508	2	US-09-627-650B-7	629	28	41.2	177	2	US-09-270-767-40943	Sequence 40943, A
557	30	44.1	2508	2	US-09-436-063C-7	630	28	41.2	177	2	US-09-270-767-56159	Sequence 56159, A
558	30	44.1	2544	2	US-09-627-650B-3	631	28	41.2	193	2	US-09-198-452A-230	Sequence 230, App
559	30	44.1	2544	2	US-09-436-063C-3	632	28	41.2	217	2	US-09-724-623-112	Sequence 112, App
560	30	44.1	2601	2	US-09-627-650B-9	633	28	41.2	242	2	US-09-252-991A-19136	Sequence 19136, A
561	30	44.1	2601	2	US-09-436-063C-9	634	28	41.2	243	2	US-09-248-796A-17137	Sequence 17137, A
562	29	42.6	27	1	US-08-451-240-19	635	28	41.2	266	2	US-09-248-796A-14391	Sequence 14391, A
563	29	42.6	27	1	US-08-451-240-19	636	28	41.2	276	2	US-09-248-796A-14595	Sequence 14595, A
564	29	42.6	27	2	US-09-154-390-35	637	28	41.2	295	2	US-09-252-991A-22401	Sequence 22401, A
565	29	42.6	27	2	US-09-154-390-36	638	28	41.2	337	2	US-09-477-962-125	Sequence 125, App
566	29	42.6	27	2	US-09-154-390-37	639	28	41.2	349	2	US-09-252-991A-3226	Sequence 3226, A
567	29	42.6	27	4	PCT-US94-12591-19	640	28	41.2	349	2	US-09-107-532A-3914	Sequence 3914, Ap
568	29	42.6	27	4	PCT-US94-12591-33	641	28	41.2	349	2	US-09-625-634A-3	Sequence 3, Appl1
569	29	42.6	29	1	US-08-451-240-18	642	28	41.2	349	2	US-09-625-634A-3	Sequence 3, Appl1
570	29	42.6	29	1	US-08-154-390-18	643	28	41.2	365	2	US-09-801-874-5	Sequence 5, Appl1
571	29	42.6	29	4	PCT-US94-12591-18	644	28	41.2	381	2	US-09-252-991A-26281	Sequence 26281, A
572	29	42.6	71	2	US-09-270-767-35140	645	28	41.2	398	2	US-09-942-991A-16217	Sequence 16217, A
573	29	42.6	71	2	US-09-270-767-50357	646	28	41.2	416	2	US-09-942-991A-16217	Sequence 7087, Ap
574	29	42.6	76	2	US-09-270-767-37686	647	28	41.2	437	2	US-09-489-039A-11439	Sequence 11439, A
575	29	42.6	76	2	US-09-270-767-52903	648	28	41.2	449	2	US-10-011-200-3	Sequence 3, Appl1
576	29	42.6	112	2	US-09-902-540-16502	649	28	41.2	451	2	US-09-602-787A-498	Sequence 498, App
577	29	42.6	120	2	US-09-252-991A-24786	650	28	41.2	481	2	US-09-248-796A-17138	Sequence 17138, A
578	29	42.6	143	2	US-09-270-767-33685	651	28	41.2	487	2	US-08-961-083-42	Sequence 42, Appl1
579	29	42.6	143	2	US-09-270-767-54902	652	28	41.2	487	2	US-09-536-784-42	Sequence 42, Appl1
580	29	42.6	154	2	US-09-270-767-39843	653	28	41.2	487	2	US-09-765-271-42	Sequence 42, Appl1
581	29	42.6	154	2	US-09-270-767-55060	654	28	41.2	487	2	US-09-765-271A-42	Sequence 42, Appl1
582	29	42.6	154	2	US-10-104-047-2931	655	28	41.2	488	2	US-09-583-110-3891	Sequence 3891, Ap
583	29	42.6	293	2	US-09-252-991A-19886	656	28	41.2	490	2	US-08-896-346-2	Sequence 2, Appl1
584	29	42.6	306	2	US-09-248-796A-15256	657	28	41.2	507	2	US-09-107-433-4015	Sequence 4015, Ap
585	29	42.6	337	2	US-09-902-540-13005	658	28	41.2	516	2	US-08-379-580-4	Sequence 4, Appl1
586	29	42.6	383	2	US-09-248-796A-26790	659	28	41.2	540	2	US-09-902-540-16745	Sequence 16745, A
587	29	42.6	392	2	US-08-311-731A-210	660	28	41.2	554	2	US-09-949-016-10978	Sequence 10978, A
588	29	42.6	443	2	US-09-489-039A-11069	661	28	41.2	595	2	US-09-252-991A-17966	Sequence 17966, A
589	29	42.6	451	2	US-09-446-681-4	662	28	41.2	684	2	US-09-489-039A-13436	Sequence 13436, A
590	29	42.6	455	2	US-09-252-991A-20384	663	28	41.2	783	2	US-09-252-991A-19688	Sequence 19688, A
591	29	42.6	456	2	US-09-328-352-5446	664	28	41.2	792	2	US-09-303-518D-185	Sequence 185, App
592	29	42.6	456	2	US-09-489-039A-8332	665	28	41.2	819	2	US-09-651-666-15	Sequence 15, Appl1
593	29	42.6	462	2	US-09-328-352-4819	666	28	41.2	819	2	US-09-650-885-15	Sequence 15, Appl1
594	29	42.6	462	2	US-09-602-787A-502	667	28	41.2	827	2	US-09-252-991A-24033	Sequence 24033, A
595	29	42.6	514	2	US-09-469-211A-3	668	28	41.2	870	1	US-08-190-687B-25	Sequence 25, Appl1
596	29	42.6	540	2	US-09-902-540-11379	669	28	41.2	880	4	PCT-US94-10198-5	Sequence 5, Appl1
597	29	42.6	543	2	US-09-252-991A-29078	670	28	41.2	870	4	US-09-538-092-1577	Sequence 577, App
598	29	42.6	545	2	US-09-572-147-2	671	28	41.2	1047	1	US-08-190-687B-8	Sequence 8, Appl1
599	29	42.6	550	2	US-09-330-245A-2	672	28	41.2	1161	2	US-09-817-762-8	Sequence 8, Appl1
600	29	42.6	550	2	US-09-614-891-7	673	28	41.2	1493	2	US-09-489-039A-13687	Sequence 13687, A
601	29	42.6	645	2	US-09-252-991A-32969	674	28	41.2	2616	2	US-09-303-518D-879	Sequence 879, App
602	29	42.6	660	2	US-09-252-991A-32871	675	28	41.2	3122	2	US-10-237-551-201	Sequence 201, App
603	29	42.6	671	1	US-07-640-029-2	676	28	41.2	3122	2	US-10-237-551-201	Sequence 250, App
604	29	42.6	817	1	US-09-538-092-739	677	28	41.2	51	2	US-09-270-767-40800	Sequence 40800, A
605	29	42.6	866	2	US-09-489-039A-10262	678	28	41.2	51	2	US-09-270-767-56016	Sequence 56016, A
606	29	42.6	907	2	US-09-252-991A-24114	679	27.5	40.4	163	2	US-09-270-767-19224	Sequence 31924, A
607	29	42.6	1044	2	US-09-252-991A-22493	680	27.5	40.4	163	2	US-09-270-767-47141	Sequence 47141, A
608	29	42.6	1180	2	US-09-252-991A-32464	681	27	39.7	30	4	PCT-US96-01720-3	Sequence 4, Appl1
609	28	41.2	17	1	US-08-025-321C-9	682	27	39.7	33	4	PCT-US96-01720-3	Sequence 3, Appl1
610	28	41.2	48	2	US-09-270-767-38501	683	27	39.7	73	2	US-09-513-999C-7202	Sequence 7202, Ap
611	28	41.2	48	2	US-09-270-767-53718	684	27	39.7	92	2	US-09-489-039A-13903	Sequence 13903, A

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686	27	39.7	101	2	US-09-252-991A-24298	Sequence 24298, A	759	27	39.7	1497	2	US-09-529-904-3	Sequence 3, Appl
687	27	39.7	129	2	US-09-134-000C-5417	Sequence 5417, Ap	760	27	39.7	1747	2	US-09-949-016-7835	Sequence 7835, Ap
688	27	39.7	127	1	US-08-482-882-45	Sequence 45, Appl	761	27	39.7	1927	2	US-09-949-016-6206	Sequence 6206, Ap
689	27	39.7	127	1	US-08-483-389-45	Sequence 45, Appl	762	27	39.7	2710	1	US-08-568-459A-12	Sequence 12, Appl
690	27	39.7	127	1	US-08-487-113D-45	Sequence 45, Appl	763	27	39.7	2710	1	US-08-487-826B-12	Sequence 12, Appl
691	27	39.7	127	1	US-08-473-503-45	Sequence 45, Appl	764	27	39.7	2710	2	US-09-210-288-12	Sequence 12, Appl
692	27	39.7	127	1	US-08-483-933-45	Sequence 45, Appl	765	27	39.7	2710	2	US-10-153-273-12	Sequence 12, Appl
693	27	39.7	127	1	US-08-720-420A-45	Sequence 45, Appl	766	27	39.7	3060	1	US-08-487-826B-14	Sequence 14, Appl
694	27	39.7	127	1	US-08-714-017-45	Sequence 45, Appl	767	27	39.7	3907	2	US-10-029-217A-24	Sequence 24, Appl
695	27	39.7	127	2	US-08-475-680-45	Sequence 45, Appl	768	27	39.7	212	2	US-08-763-121-1	Sequence 1, Appl
696	27	39.7	132	2	US-09-248-796A-22903	Sequence 22903, A	769	27	39.0	212	2	US-09-216-066-1	Sequence 1, Appl
697	27	39.7	138	2	US-09-270-767-61321	Sequence 61321, A	770	27	39.0	477	2	US-09-118-324-2	Sequence 2, Appl
698	27	39.7	157	1	US-08-599-602-2	Sequence 2, Appl	771	27	39.0	485	1	US-08-453-956-15	Sequence 15, Appl
699	27	39.7	157	1	US-09-197-816-2	Sequence 2, Appl	772	27	39.0	485	1	US-08-086-631-15	Sequence 15, Appl
700	27	39.7	163	2	US-09-252-991A-29098	Sequence 29098, A	773	27	39.0	485	1	US-08-452-930-15	Sequence 15, Appl
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702	27	39.7	205	2	US-09-540-236-3658	Sequence 3658, Ap	775	27	39.0	485	4	PCR-UE93-08174-15	Sequence 15, Appl
703	27	39.7	232	2	US-09-252-991A-26247	Sequence 26247, A	776	27	39.0	642	2	US-09-252-991A-21889	Sequence 21889, A
704	27	39.7	234	2	US-09-252-991A-25162	Sequence 25162, A	777	27	38.2	29	2	US-09-270-767-56788	Sequence 56788, A
705	27	39.7	275	2	US-09-328-352-7552	Sequence 7552, Ap	778	27	38.2	41	1	US-07-924-753-1	Sequence 1, Appl
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707	27	39.7	291	2	US-09-270-767-33003	Sequence 33003, A	780	27	38.2	54	1	US-08-563-148E-1	Sequence 1, Appl
708	27	39.7	297	2	US-09-252-991A-27478	Sequence 27478, A	781	27	38.2	57	2	US-09-513-999C-7481	Sequence 7481, Ap
709	27	39.7	300	2	US-09-949-016-10727	Sequence 10727, A	782	27	38.2	59	2	US-09-230-637-47	Sequence 47, Appl
710	27	39.7	313	2	US-09-800-729-156	Sequence 196, App	783	27	38.2	70	1	US-08-009-265-30	Sequence 30, Appl
711	27	39.7	318	2	US-09-489-847-328	Sequence 328, App	784	27	38.2	70	1	US-08-002-263-32	Sequence 32, Appl
712	27	39.7	326	2	US-09-884-570-8	Sequence 8, Appl	785	27	38.2	70	1	US-08-682-485A-21	Sequence 21, Appl
713	27	39.7	336	2	US-10-157-457A-8	Sequence 8, Appl	786	27	38.2	70	1	US-08-682-485A-22	Sequence 22, Appl
714	27	39.7	333	2	US-09-562-737-4	Sequence 4, Appl	787	27	38.2	70	1	US-08-682-485A-23	Sequence 23, Appl
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716	27	39.7	351	2	US-09-198-452A-733	Sequence 733, App	789	27	38.2	70	1	US-08-933-314-22	Sequence 22, Appl
717	27	39.7	351	2	US-09-438-185A-695	Sequence 695, App	790	27	38.2	70	1	US-08-933-314-22	Sequence 22, Appl
718	27	39.7	379	2	US-09-402-532-1	Sequence 1, Appl	791	27	38.2	70	2	US-08-933-314-23	Sequence 23, Appl
719	27	39.7	382	2	US-09-402-532-4	Sequence 4, Appl	792	27	38.2	71	2	US-08-472-053-45	Sequence 45, Appl
720	27	39.7	396	2	US-09-107-532A-4277	Sequence 4277, Ap	793	27	38.2	71	2	US-08-472-053-48	Sequence 48, Appl
721	27	39.7	397	2	US-09-270-767-45798	Sequence 45798, A	794	27	38.2	71	6	5177308-1	APPLICANT, BBR
722	27	39.7	407	2	US-09-328-352-5318	Sequence 5318, Ap	795	27	38.2	77	2	US-09-513-999C-5531	Sequence 5531, Ap
723	27	39.7	411	2	US-09-540-236-2952	Sequence 2952, Ap	796	27	38.2	82	2	US-09-144-776B-18	Sequence 18, Appl
724	27	39.7	419	2	US-09-402-532-2	Sequence 2, Appl	797	27	38.2	82	2	US-08-882-431B-18	Sequence 18, Appl
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726	27	39.7	412	2	US-09-999-833A-157	Sequence 157, App	799	27	38.2	84	2	US-09-270-767-51969	Sequence 51969, A
727	27	39.7	412	2	US-10-020-445A-157	Sequence 157, App	800	27	38.2	89	2	US-08-472-053-47	Sequence 47, Appl
728	27	39.7	414	2	US-09-402-532-5	Sequence 5, Appl	801	27	38.2	90	2	US-09-621-976-5404	Sequence 5404, Ap
729	27	39.7	420	2	US-09-949-016-9364	Sequence 9364, Ap	802	27	38.2	93	2	US-09-621-976-4468	Sequence 4468, Ap
730	27	39.7	420	2	US-10-070-634-12	Sequence 12, Appl	803	27	38.2	93	2	US-09-270-767-36229	Sequence 36229, A
731	27	39.7	423	2	US-09-328-352-5667	Sequence 5667, Ap	804	27	38.2	93	2	US-09-270-767-51446	Sequence 51446, A
732	27	39.7	425	2	US-09-711-164-428	Sequence 428, App	805	27	38.2	94	1	US-08-150-203A-6	Sequence 6, Appl
733	27	39.7	433	2	US-09-328-352-6503	Sequence 6503, Ap	806	27	38.2	94	1	US-08-451-472-23	Sequence 6, Appl
734	27	39.7	444	2	US-09-402-532-7	Sequence 7, Appl	807	27	38.2	94	2	US-08-949-788-6	Sequence 6, Appl
735	27	39.7	444	2	US-09-543-681A-6293	Sequence 6293, Ap	808	27	38.2	95	2	US-09-621-976-4670	Sequence 4670, Ap
736	27	39.7	454	2	US-09-248-796A-18402	Sequence 18402, A	809	27	38.2	98	2	US-09-194-139-9	Sequence 9, Appl
737	27	39.7	469	2	US-09-134-000C-5065	Sequence 5065, Ap	810	27	38.2	100	1	US-09-047-125-27	Sequence 27, Appl
738	27	39.7	470	2	US-09-328-352-6673	Sequence 6673, Ap	811	27	38.2	100	2	US-07-736-335E-47	Sequence 27, Appl
739	27	39.7	471	2	US-09-106-464-2	Sequence 2, Appl	812	27	38.2	100	2	US-09-248-796A-23040	Sequence 23040, A
740	27	39.7	475	2	US-09-248-796A-15218	Sequence 15218, A	813	27	38.2	108	1	US-08-451-472-23	Sequence 23, Appl
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742	27	39.7	509	2	US-09-248-796A-20031	Sequence 20031, A	815	27	38.2	109	2	US-09-270-767-33071	Sequence 33071, A
743	27	39.7	513	2	US-09-252-991A-19670	Sequence 19670, A	816	27	38.2	109	2	US-09-270-767-48288	Sequence 48288, A
744	27	39.7	521	1	US-08-504-048-9	Sequence 9, Appl	817	27	38.2	110	2	US-09-614-912-10	Sequence 10, Appl
745	27	39.7	537	1	US-08-647-397-2	Sequence 2, Appl	818	27	38.2	120	2	US-09-569-611C-32	Sequence 32, Appl
746	27	39.7	537	2	US-09-949-016-5954	Sequence 5954, Ap	819	27	38.2	122	2	US-09-569-611C-31	Sequence 31, Appl
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748	27	39.7	546	2	US-09-614-891-8	Sequence 8, Appl	821	27	38.2	128	2	US-09-244-796A-27548	Sequence 27548, A
749	27	39.7	547	2	US-09-949-016-7043	Sequence 7043, Ap	822	27	38.2	129	2	US-09-252-991A-22304	Sequence 22304, A
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755	27	39.7	902	2	US-09-134-000C-6743	Sequence 6743, Ap	828	27	38.2	145	2	US-09-902-540-15418	Sequence 15418, A
756	27	39.7	1269	2	US-09-902-540-15558	Sequence 15558, A	829	27	38.2	146	2	US-09-602-787A-610	Sequence 610, App
757	27	39.7	1461	2	US-10-142-231-86	Sequence 86, Appl	830	27	38.2	151	1	US-08-563-148E-6	Sequence 6, Appl

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832	26	38.2	151	2	US-09-489-039A-11146	Sequence 1146, A	905	26	38.2	337	2	US-09-477-96C-119	Sequence 119, App
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834	26	38.2	151	2	US-09-868-953A-1	Sequence 1, Appl1	907	26	38.2	346	2	US-09-807-933B-11	Sequence 11, Appl
835	26	38.2	151	2	US-09-668-953A-2	Sequence 2, Appl1	908	26	38.2	351	2	US-09-614-912-8	Sequence 8, Appl1
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839	26	38.2	169	2	US-09-569-611C-29	Sequence 29, Appl	912	26	38.2	360	2	US-09-252-991A-29684	Sequence 29684, A
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841	26	38.2	178	1	US-08-463-262A-6	Sequence 6, Appl1	914	26	38.2	370	2	US-09-614-912-2	Sequence 4, Appl1
842	26	38.2	178	1	US-08-463-989-6	Sequence 6, Appl1	915	26	38.2	378	2	US-09-487-558B-330	Sequence 330, App
843	26	38.2	178	1	US-09-003-574-6	Sequence 6, Appl1	916	26	38.2	379	2	US-09-402-532-3	Sequence 3, Appl1
844	26	38.2	178	2	US-09-003-570-6	Sequence 6, Appl1	917	26	38.2	401	2	US-09-489-039A-12481	Sequence 12481, A
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850	26	38.2	191	1	US-08-463-989-3	Sequence 3, Appl1	923	26	38.2	416	2	US-09-962-955D-38	Sequence 38, Appl1
851	26	38.2	191	2	US-09-003-574-3	Sequence 3, Appl1	924	26	38.2	421	2	US-09-489-039A-10507	Sequence 10507, A
852	26	38.2	191	2	US-09-003-570-3	Sequence 3, Appl1	925	26	38.2	426	2	US-09-489-039A-9805	Sequence 9805, Ap
853	26	38.2	191	2	US-09-864-541A-3	Sequence 3, Appl1	926	26	38.2	432	1	US-08-700-152A-4	Sequence 4, Appl1
854	26	38.2	191	2	US-09-270-767-44048	Sequence 44048, A	927	26	38.2	432	2	US-09-248-796A-16450	Sequence 16450, A
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856	26	38.2	207	2	US-09-489-039A-9689	Sequence 9689, Ap	929	26	38.2	451	2	US-09-252-991A-25804	Sequence 25804, A
857	26	38.2	213	2	US-09-252-991A-20163	Sequence 20163, A	930	26	38.2	451	2	US-08-591-466-22	Sequence 22, Appl
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859	26	38.2	219	1	US-08-816-605-2	Sequence 2, Appl1	932	26	38.2	452	4	PCT-US94-06430-22	Sequence 22, Appl
860	26	38.2	222	1	US-09-252-991A-24147	Sequence 24147, A	933	26	38.2	457	2	US-09-543-681A-6044	Sequence 6044, Ap
861	26	38.2	228	2	US-08-896-933-25	Sequence 25, Appl	934	26	38.2	462	2	US-09-328-352-5497	Sequence 5497, Ap
862	26	38.2	228	2	US-09-314-235-25	Sequence 25, Appl	935	26	38.2	464	2	US-09-693-746-14	Sequence 14, Appl
863	26	38.2	228	2	US-09-708-008B-25	Sequence 25, Appl	936	26	38.2	468	2	US-09-004-868-121	Sequence 121, App
864	26	38.2	236	2	US-09-216-430C-14	Sequence 14, Appl	937	26	38.2	471	2	US-09-311-626B-8	Sequence 8, Appl1
865	26	38.2	246	2	US-09-252-991A-23985	Sequence 23985, A	938	26	38.2	476	2	US-09-673-300-10	Sequence 10, Appl
866	26	38.2	254	2	US-09-252-991A-24540	Sequence 24540, A	939	26	38.2	495	2	US-09-248-796A-14275	Sequence 14275, A
867	26	38.2	255	1	US-08-236-918A-8	Sequence 8, Appl1	940	26	38.2	517	1	US-08-485-241-5	Sequence 5, Appl1
868	26	38.2	255	1	US-08-816-605-9	Sequence 9, Appl1	941	26	38.2	517	1	US-08-874-162-5	Sequence 5, Appl1
869	26	38.2	255	2	US-09-006-353A-11	Sequence 11, Appl	942	26	38.2	518	1	US-08-299-675-2	Sequence 2, Appl1
870	26	38.2	255	2	US-09-007-097-2	Sequence 2, Appl1	943	26	38.2	518	1	US-08-485-241-3	Sequence 3, Appl1
871	26	38.2	255	2	US-09-150-864A-8	Sequence 8, Appl1	944	26	38.2	518	1	US-08-874-162-3	Sequence 3, Appl1
872	26	38.2	255	2	US-09-573-986-11	Sequence 11, Appl	945	26	38.2	539	1	US-08-759-581B-20	Sequence 20, Appl
873	26	38.2	255	2	US-09-578-764A-2	Sequence 2, Appl1	946	26	38.2	539	2	US-09-304-711-20	Sequence 20, Appl
874	26	38.2	255	2	US-09-623-545A-2	Sequence 2, Appl1	947	26	38.2	539	2	US-09-173-281-20	Sequence 20, Appl
875	26	38.2	255	2	US-09-877-338-2	Sequence 2, Appl1	948	26	38.2	546	2	US-09-252-991A-17104	Sequence 17104, A
876	26	38.2	255	4	PCT-US96-03965-8	Sequence 8, Appl1	949	26	38.2	566	2	US-09-252-991A-18531	Sequence 18531, A
877	26	38.2	258	2	US-09-252-991A-32929	Sequence 32929, A	950	26	38.2	609	2	US-09-252-991A-32547	Sequence 32547, A
878	26	38.2	260	2	US-09-270-767-45786	Sequence 45786, A	951	26	38.2	626	2	US-09-248-796A-27023	Sequence 27023, A
879	26	38.2	262	2	US-09-270-767-41775	Sequence 41775, A	952	26	38.2	638	1	US-08-463-262A-11	Sequence 11, Appl
880	26	38.2	261	2	US-09-540-236-2069	Sequence 2069, Ap	953	26	38.2	638	1	US-08-463-969-11	Sequence 11, Appl
881	26	38.2	271	2	US-09-569-611C-30	Sequence 30, Appl	954	26	38.2	638	2	US-09-003-574-11	Sequence 11, Appl
882	26	38.2	272	2	US-09-949-016-7520	Sequence 7520, Ap	955	26	38.2	638	2	US-09-003-570-31	Sequence 31, Appl
883	26	38.2	276	2	US-09-252-991A-25159	Sequence 25159, A	956	26	38.2	638	2	US-09-864-541A-31	Sequence 11, Appl
884	26	38.2	279	2	US-09-252-991A-18598	Sequence 18598, A	957	26	38.2	652	2	US-09-252-991A-13855	Sequence 13855, A
885	26	38.2	286	2	US-09-270-767-35905	Sequence 35905, A	958	26	38.2	666	2	US-09-050-729-70	Sequence 70, Appl
886	26	38.2	286	2	US-09-270-767-51122	Sequence 51122, A	959	26	38.2	692	2	US-09-003-574-31	Sequence 31, Appl
887	26	38.2	288	1	US-08-368-852-15	Sequence 15, Appl	960	26	38.2	692	2	US-09-864-541A-31	Sequence 31, Appl
888	26	38.2	288	1	US-08-525-940-15	Sequence 15, Appl	961	26	38.2	717	2	US-09-489-039A-9547	Sequence 9547, Ap
889	26	38.2	288	1	US-08-976-838-15	Sequence 15, Appl	962	26	38.2	720	2	US-09-756-071B-20	Sequence 20, Appl
890	26	38.2	291	2	US-09-252-991A-30666	Sequence 30666, A	963	26	38.2	726	1	US-08-313-185-49	Sequence 49, Appl
891	26	38.2	293	2	US-09-252-991A-26106	Sequence 26106, A	964	26	38.2	726	1	US-08-459-499-13	Sequence 13, Appl
892	26	38.2	298	2	US-08-767-942A-25	Sequence 25, Appl	965	26	38.2	726	1	US-09-082-614A-49	Sequence 49, Appl
893	26	38.2	298	2	US-09-177-165A-23	Sequence 23, Appl	966	26	38.2	726	1	US-09-489-039A-9547	Sequence 9547, Ap
894	26	38.2	298	2	US-09-917-254-61	Sequence 61, Appl	967	26	38.2	735	2	US-08-525-991A-30503	Sequence 30503, A
895	26	38.2	308	2	US-09-050-739-94	Sequence 94, Appl	968	26	38.2	799	1	US-08-976-838-21	Sequence 21, Appl
896	26	38.2	309	2	US-09-252-991A-25386	Sequence 25386, A	969	26	38.2	881	1	US-08-525-991A-31	Sequence 31, Appl
897	26	38.2	310	2	US-09-252-991A-25177	Sequence 25177, A	970	26	38.2	881	1	US-08-976-838-21	Sequence 21, Appl
898	26	38.2	310	2	US-09-252-991A-28514	Sequence 28514, A	971	26	38.2	909	2	US-08-525-991A-18	Sequence 18, Appl
899	26	38.2	310	2	US-09-107-532A-3732	Sequence 3732, Ap	972	26	38.2	915	1	US-08-976-838-18	Sequence 18, Appl
900	26	38.2	311	2	US-09-252-991A-22857	Sequence 22857, A	973	26	38.2	915	2	US-09-214-555B-2	Sequence 2, Appl1
901	26	38.2	317	2	US-09-134-000C-5669	Sequence 5669, Ap	974	26	38.2				
902	26	38.2	320	2	US-09-270-767-34209	Sequence 34209, A	975	26	38.2				
903	26	38.2	320	2	US-09-270-767-49426	Sequence 49426, A	976	26	38.2				

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977 26 38.2 915 2 US-09-214-5558-7 Sequence 7, Appl
978 26 38.2 920 2 US-09-919-039-76 Sequence 76, Appl
979 26 38.2 953 2 US-09-252-991A-30039 Sequence 30039, A
980 26 38.2 1032 2 US-09-252-991A-24058 Sequence 24058, A
981 26 38.2 1064 1 US-08-537-210A-3 Sequence 3, Appl
982 26 38.2 1064 1 US-08-537-210A-3 Sequence 3, Appl
983 26 38.2 1106 2 US-09-949-016-9666 Sequence 9666, Ap
984 26 38.2 1147 1 US-08-144-121-3 Sequence 3, Appl
985 26 38.2 1147 1 US-08-735-893-3 Sequence 3, Appl
986 26 38.2 1147 2 US-10-841-139-3 Sequence 3, Appl
987 26 38.2 1153 2 US-09-560-385A-16 Sequence 16, Appl
988 26 38.2 1155 2 US-09-560-385A-24 Sequence 24, Appl
989 26 38.2 1165 1 US-08-144-121-2 Sequence 2, Appl
990 26 38.2 1165 1 US-08-735-893-2 Sequence 2, Appl
991 26 38.2 1165 2 US-10-841-139-2 Sequence 2, Appl
992 26 38.2 1167 2 US-09-560-385A-20 Sequence 20, Appl
993 26 38.2 1170 2 US-09-561-709B-12 Sequence 12, Appl
994 26 38.2 1170 2 US-09-560-385A-14 Sequence 14, Appl
995 26 38.2 1172 2 US-09-919-172-16 Sequence 16, Appl
996 26 38.2 1174 2 US-09-560-385A-22 Sequence 22, Appl
997 26 38.2 1180 2 US-09-543-681A-6436 Sequence 6436, Ap
998 26 38.2 1186 2 US-09-560-385A-18 Sequence 18, Appl
999 26 38.2 1404 2 US-09-345-473E-24 Sequence 24, Appl
1000 26 38.2 1404 2 US-09-862-027-24 Sequence 24, Appl
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ALIGNMENTS

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RESULT 1
US-09-579-883A-13
; Sequence 13, Application US/09579883A
; Patent No. 6686443
; GENERAL INFORMATION:
; APPLICANT: RABENSTEIN, DALLAS
; APPLICANT: SHI, TIESHENG
; TITLE OF INVENTION: CHEMICAL REAGENTS FOR FORMATION OF DISULFIDE BONDS IN PEPTIDES
; FILE REFERENCE: 407T-891100US
; CURRENT APPLICATION NUMBER: US/09/579,883A
; CURRENT FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-579-883A-13

Query Match      82.4%; Score 56; DB 2; Length 20;
Best Local Similarity 58.8%; Pred. No. 4.6e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXXGC 17
      ||| ||| ||| ||| |||
Db      1 CFGSRIDRIGAGSGMGC 17

RESULT 2
US-09-623-548A-469
; Sequence 469, Application US/09623548A
; Patent No. 66849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
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; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 469
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-469
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Query Match      82.4%; Score 56; DB 2; Length 20;
Best Local Similarity 58.8%; Pred. No. 4.6e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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QY      1 CFGXXXDRIGXXSXXGC 17
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Db      1 CFGSRIDRIGAGSGMGC 17
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RESULT 3
US-09-657-276-469
; Sequence 469, Application US/09657276
; Patent No. 6687470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 469
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-469

Query Match      82.4%; Score 56; DB 2; Length 20;
Best Local Similarity 58.8%; Pred. No. 4.6e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXXGC 17
      ||| ||| ||| ||| |||
Db      1 CFGSRIDRIGAGSGMGC 17

RESULT 4
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US-09-623-548A-470
; Sequence 470, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 470
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-623-548A-470

Query Match 82.4%; Score 56; DB 2; Length 21;
Best Local Similarity 58.8%; Pred. No. 4.8e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 CFCGXXDRIGXXSXXGC 17
Db 1 CFCGRIDRIGAGSGMGC 17

RESULT 5
US-09-657-276-470
; Sequence 470, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 470
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Peptide
US-09-657-276-470

Query Match 82.4%; Score 56; DB 2; Length 21;
Best Local Similarity 58.8%; Pred. No. 4.8e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFCGXXDRIGXXSXXGC 17
Db 1 CFCGRIDRIGAGSGMGC 17

RESULT 6
5212286-43
; Patent No. 5212286
; APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
; PEPTIDE COMPOUNDS
; NUMBER OF SEQUENCES: 68
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/870,795
; FILING DATE: 05-JUN-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 766,030
; FILING DATE: 08-MAY-1985
; APPLICATION NUMBER: 602,117
; FILING DATE: 09-APR-1984
; APPLICATION NUMBER: 616,488
; FILING DATE: 01-JUN-1984
; SEQ ID NO:43
; LENGTH: 23
5212286-43

Query Match 82.4%; Score 56; DB 6; Length 23;
Best Local Similarity 58.8%; Pred. No. 5.3e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFCGXXDRIGXXSXXGC 17
Db 2 CFCGRIDRIGAGSALGC 18

RESULT 7
5212286-47
; Patent No. 5212286
; APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
; PEPTIDE COMPOUNDS
; NUMBER OF SEQUENCES: 68
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/870,795
; FILING DATE: 05-JUN-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 766,030
; FILING DATE: 08-MAY-1985
; APPLICATION NUMBER: 602,117
; FILING DATE: 09-APR-1984
; APPLICATION NUMBER: 616,488
; FILING DATE: 01-JUN-1984
; SEQ ID NO:47
; LENGTH: 23
5212286-47

Query Match 82.4%; Score 56; DB 6; Length 23;
Best Local Similarity 58.8%; Pred. No. 5.3e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFCGXXDRIGXXSXXGC 17
Db 2 CFCGRIDRIGAGSALGC 18

RESULT 8

US-07-754-958-4
; Sequence 4, Application US/07754958
; Patent No. 5336759
; GENERAL INFORMATION:
; APPLICANT: MATSUO, HISAYUKI
; APPLICANT: KANGAWA, KENJI
; APPLICANT: MINAMINO, NAOTO
; TITLE OF INVENTION: A NOVEL BIOLOGICALLY ACTIVE PEPTIDE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/754,958
; FILING DATE: 19910904
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T
; REGISTRATION NUMBER: 56281
; REFERENCE/DOCKET NUMBER: 9437/92322
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-754-958-4
Query Match 82.4%; Score 56; DB 1; Length 24;
Best Local Similarity 58.8%; Pred. No. 5.6e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 CFGXXXDRIGXXSXGC 17
||| ||| |||
Db 4 CFGSRIDRIGAGSGMGC 20
RESULT 9
US-07-754-947-4
; Sequence 4, Application US/07754947
; Patent No. 5338830
; GENERAL INFORMATION:
; APPLICANT: MATSUO, HISAYUKI
; APPLICANT: KANGAWA, KENJI
; APPLICANT: MINAMINO, NAOTO
; TITLE OF INVENTION: A NOVEL BIOLOGICALLY ACTIVE PEPTIDE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1625 L STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

US-07-754-947-4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/754,947
; FILING DATE: 19910904
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: 5683/92321
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3067
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-754-947-4
Query Match 82.4%; Score 56; DB 1; Length 24;
Best Local Similarity 58.8%; Pred. No. 5.6e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 CFGXXXDRIGXXSXGC 17
||| ||| |||
Db 4 CFGSRIDRIGAGSGMGC 20
RESULT 10
US-09-623-548A-468
; Sequence 468, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 468
; LENGTH: 24
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-468
Query Match 82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 5.6e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 CFGXXXDRIGXXSXGC 17
||| ||| |||
Db 4 CFGSRIDRIGAGSGMGC 20


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RESULT 11
US-09-623-548A-471
; Sequence 471, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 471
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-623-548A-471

Query Match      82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 5.6e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXDXDRIGXXSXGC 17
      ||| ||| ||| |||
DB      4 CFGSRIDRIGAGSGWGC 20

RESULT 12
US-09-657-276-468
; Sequence 468, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 468
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-657-276-471
```

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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-468

Query Match      82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 5.6e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXDXDRIGXXSXGC 17
      ||| ||| ||| |||
DB      4 CFGSRIDRIGAGSGWGC 20

RESULT 13
US-09-657-276-471
; Sequence 471, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 471
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-657-276-471

Query Match      82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 5.6e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXDXDRIGXXSXGC 17
      ||| ||| ||| |||
DB      4 CFGSRIDRIGAGSGWGC 20

RESULT 14
5212286-31
; Patent No. 5212286
; APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: ATRIAL NUTRIURETIC/VASODILATOR
; PEPTIDE COMPOUNDS
; NUMBER OF SEQUENCES: 68
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/870,795
; FILING DATE: 05-JUN-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 766,030
; FILING DATE: 08-MAY-1985
; APPLICATION NUMBER: 602,117
; FILING DATE: 09-APR-1984
; APPLICATION NUMBER: 616,488
; FILING DATE: 01-JUN-1984
```

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;SEQ ID NO:31:
; LENGTH: 25
5212286-31

Query Match      82.4%; Score 56; DB 6; Length 25;
Best Local Similarity 58.8%; Pred. No. 5.8e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
   ||| ||| ||| |||
Db 4 CFGGRIDRIGASALGC 20

RESULT 15
5212286-35
; Patent No. 5212286
; APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
; PEPTIDE COMPOUNDS
; NUMBER OF SEQUENCES: 68
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/870,795
; FILING DATE: 05-JUN-1986
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 766,030
; FILING DATE: 08-MAY-1985
; APPLICATION NUMBER: 602,117
; FILING DATE: 09-APR-1984
; APPLICATION NUMBER: 616,488
; FILING DATE: 01-JUN-1984
; SEQ ID NO:35:
; LENGTH: 25
5212286-35

Query Match      82.4%; Score 56; DB 6; Length 25;
Best Local Similarity 58.8%; Pred. No. 5.8e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
   ||| ||| ||| |||
Db 4 CFGARIDRIGASGLGC 20

RESULT 16
US-08-451-240-14
; Sequence 14, Application US/08451240
; Patent No. 5665704
; GENERAL INFORMATION:
; APPLICANT: Lowe, David
; APPLICANT: Cunningham, Brian
; APPLICANT: Gare, David
; APPLICANT: McDowell, Robert S.
; APPLICANT: Burnier, John
; TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC
; TITLE OF INVENTION: PEPTIDES
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,240
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
```

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; APPLICATION NUMBER: 08/362552
; FILING DATE: 06-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/152994
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0844P1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-451-240-14

Query Match      82.4%; Score 56; DB 1; Length 28;
Best Local Similarity 58.8%; Pred. No. 6.5e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
   ||| ||| ||| |||
Db 7 CFGKMDRIGASGLGC 23

RESULT 17
US-08-470-846A-14
; Sequence 14, Application US/08470846A
; Patent No. 5846932
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Lowe, David G.
; APPLICANT: Cunningham, Brian C.
; APPLICANT: Gare, David
; APPLICANT: McDowell, Robert S.
; APPLICANT: Burnier, John
; TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC PEPTIDES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,846A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/419877
; FILING DATE: 11-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/362552
; FILING DATE: 06-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/152994
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0844P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
```

TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-470-846A-14

Query Match 82.4%; Score 56; DB 1; Length 28;
Best Local Similarity 58.8%; Pred. No. 6.5e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 CFGXXXDRIGKXXSXXGC 17
||| ||| ||| ||| |||
Db 7 CFGKSMDRIGAGSLGC 23

RESULT 18
US-09-154-390-14
Sequence 14, Application US/09154390
Patent No. 6525022
GENERAL INFORMATION:
APPLICANT: Lowe, David G.
APPLICANT: Cunningham, Brian C.
APPLICANT: Oare, David
APPLICANT: McDowell, Robert S.
APPLICANT: Burnier, John P.
TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC PEPTIDES
FILE REFERENCE: 13734.1USWS
CURRENT APPLICATION NUMBER: US/09/154,390
CURRENT FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: US 08/470,846
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/419,877
PRIOR FILING DATE: 1995-04-11
PRIOR APPLICATION NUMBER: US 08/362,552
PRIOR FILING DATE: 1995-01-06
PRIOR APPLICATION NUMBER: PCT/US94/12591
PRIOR FILING DATE: 1994-11-04
PRIOR APPLICATION NUMBER: US 08/152,994
PRIOR FILING DATE: 1993-11-12
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-154-390-14

Query Match 82.4%; Score 56; DB 2; Length 28;
Best Local Similarity 58.8%; Pred. No. 6.5e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 CFGXXXDRIGKXXSXXGC 17
||| ||| ||| ||| |||
Db 7 CFGKSMDRIGAGSLGC 23

RESULT 19
PCT-US94-12591-14
Sequence 14, Application PC/TUS9412591
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Lowe, David
APPLICANT: Cunningham, Brian C.
APPLICANT: Oare, David
APPLICANT: McDowell, Robert S.
APPLICANT: Burnier, John
TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC
PEPTIDES

NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12591
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/152994
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Daryl B.
REGISTRATION NUMBER: 32,637
REFERENCE/DOCKET NUMBER: 844P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1249
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US94-12591-14

Query Match 82.4%; Score 56; DB 4; Length 28;
Best Local Similarity 58.8%; Pred. No. 6.5e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 CFGXXXDRIGKXXSXXGC 17
||| ||| ||| ||| |||
Db 7 CFGKSMDRIGAGSLGC 23

RESULT 20
US-09-623-548A-472
Sequence 472, Application US/09623548A
Patent No. 6849714
GENERAL INFORMATION:
APPLICANT: Conjuchem, Inc.
APPLICANT: Bridon, Dominique
APPLICANT: Ezrin, Alan
APPLICANT: Milner, Peter
APPLICANT: Holmes, Darren
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
COMPONENTS
FILE REFERENCE: 2110
CURRENT APPLICATION NUMBER: US/09/623,548A
CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 472
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence

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;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-472

Query Match
Beet Local Similarity 82.4%; Score 56; DB 2; Length 30;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXXXGC 17
   ||| ||| ||| |||
Db 11 CFGSRIDRIGAGSGMGC 27

RESULT 21
US-09-657-276-472
; Sequence 472, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 472
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-472

Query Match
Beet Local Similarity 82.4%; Score 56; DB 2; Length 30;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXXXGC 17
   ||| ||| ||| |||
Db 11 CFGSRIDRIGAGSGMGC 27

RESULT 22
US-07-828-450-7
; Sequence 7, Application US/07828450
; Patent No. 5434133
; GENERAL INFORMATION:
; APPLICANT: TANAKA, SHOUJI
; APPLICANT: MINAMITAKE, YOSHIIHARU
; APPLICANT: KITAJIMA, YASUO
; APPLICANT: FURUYA, MAYUMI
; APPLICANT: MATSUO, HISAYUKI
; TITLE OF INVENTION: CNP ANALOG PEPTIDES AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1625 L STREET, N.W.
; CITY: WASHINGTON

```

```

;
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/828,450
; FILING DATE: 19920131
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: 9437/94133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3067
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-828-450-7

Query Match
Beet Local Similarity 80.9%; Score 55; DB 1; Length 17;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXXXGC 17
   ||| ||| ||| |||
Db 1 CFGSLDRIGSGMGLGC 17

RESULT 23
US-08-737-927-1
; Sequence 1, Application US/08737927
; Patent No. 5767239
; GENERAL INFORMATION:
; APPLICANT: IMMER, Hansueli
; APPLICANT: FORSSMANN, Wolf-Georg
; APPLICANT: ADERMANN, Knut
; APPLICANT: KLESSEN, Christian
; TITLE OF INVENTION: PROCESS AND INTERMEDIATE PRODUCTS FOR
; TITLE OF INVENTION: PREPARING CARDIODILATIN FRAGMENTS, AND HIGHLY PURIFIED
; TITLE OF INVENTION: CARDIODILATIN FRAGMENTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelestein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,927
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 95/33769
; FILING DATE: 14-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Klets, Monica C.
; REGISTRATION NUMBER: 36,105

```

REFERENCE/DOCKET NUMBER: P1614-6052
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-737-927-1

Query Match 80.9%; Score 55; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 6.3e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXXRIGXXSXXGC 17
Db 1 CFGGRMDRIGAGSLGCG 17

RESULT 24
US-08-850-910A-15
Sequence 15, Application US/08850910A
Patent No. 5948761
GENERAL INFORMATION:
APPLICANT: SEILHAMER, J.J.
APPLICANT: LEWICKI, J.
APPLICANT: SCARBOROUGH, R.M.
TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIURETIC PEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER, LLP
STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: PasteSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,910A
FILING DATE: 05-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/477,226
FILING DATE: 08-FEB-1990
APPLICATION NUMBER: 07/299,880
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206,470
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200,383
FILING DATE: 31-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 219002025212
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-850-910A-15

Query Match 80.9%; Score 55; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 6.3e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXXRIGXXSXXGC 17
Db 1 CFGGRMDRIGAGSLGCG 17

RESULT 25
US-09-623-548A-474
Sequence 474, Application US/09623548A
Patent No. 6849714
GENERAL INFORMATION:
APPLICANT: Conjuchem, Inc.
APPLICANT: Bridon, Dominique
APPLICANT: Ezrin, Alan
APPLICANT: Milner, Peter
APPLICANT: Holmes, Darren
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
FILE REFERENCE: 2110
CURRENT APPLICATION NUMBER: US/09/623,548A
CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 474
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-623-548A-474

Query Match 80.9%; Score 55; DB 2; Length 17;
Best Local Similarity 58.8%; Pred. No. 6.3e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXXRIGXXSXXGC 17
Db 1 CFGGRMDRIGAGSLGCG 17

RESULT 26
US-09-657-276-474
Sequence 474, Application US/09657276
Patent No. 6887470
GENERAL INFORMATION:
APPLICANT: Conjuchem, Inc.
APPLICANT: Bridon, Dominique
APPLICANT: Ezrin, Alan
APPLICANT: Milner, Peter
APPLICANT: Holmes, Darren
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
FILE REFERENCE: 2110
CURRENT APPLICATION NUMBER: US/09/657,276
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR FILING DATE: 1999-05-17

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; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 474
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-474

Query Match      80.9%; Score 55; DB 2; Length 17;
Best Local Similarity 58.8%; Pred. No. 6.3e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXGC 17
      ||| ||| ||| |||
Db      1 CFGGRMDRIGAGSLGCG 17

RESULT 27
US-09-902-517-15
; Sequence 15, Application US/09902517
; Patent No. 6897030
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Lewicki, John
; APPLICANT: Scarborough, Robert M.
; APPLICANT: Porter, Gordon J.
; TITLE OF INVENTION: IMMUNOASSAYS FOR HUMAN AND CANINE BRAIN
; FILE REFERENCE: 219002025213
; CURRENT APPLICATION NUMBER: US/09/902,517
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 09/287,892
; PRIOR FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: 08/850,910
; PRIOR FILING DATE: 1997-05-05
; PRIOR APPLICATION NUMBER: 07/477,226
; PRIOR FILING DATE: 1990-02-08
; PRIOR APPLICATION NUMBER: 07/299,880
; PRIOR FILING DATE: 1989-01-19
; PRIOR APPLICATION NUMBER: 07/206,470
; PRIOR FILING DATE: 1988-06-14
; PRIOR APPLICATION NUMBER: 07/200,383
; PRIOR FILING DATE: 1988-05-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Proviso formula (1)
US-09-902-517-15

Query Match      80.9%; Score 55; DB 2; Length 17;
Best Local Similarity 58.8%; Pred. No. 6.3e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXGC 17
      ||| ||| ||| |||
Db      1 CFGGRMDRIGSLGCG 17

RESULT 28
US-08-850-910A-32
; Sequence 32, Application US/08850910A
; Patent No. 5948761
```

```

; GENERAL INFORMATION:
; APPLICANT: SEILHAMER, J.J.
; APPLICANT: LEWICKI, J.
; APPLICANT: SCARBOROUGH, R.M.
; TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
; TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIURETIC PEPTIDE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER, LLP
; STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/850,910A
; FILING DATE: 05-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/477,226
; FILING DATE: 08-FEB-1990
; APPLICATION NUMBER: 07/299,880
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 07/206,470
; FILING DATE: 14-JUN-1988
; APPLICATION NUMBER: 07/200,383
; FILING DATE: 31-MAY-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 219002025212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
US-08-850-910A-32

Query Match      80.9%; Score 55; DB 1; Length 20;
Best Local Similarity 58.8%; Pred. No. 7.4e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXGC 17
      ||| ||| ||| |||
Db      3 CFGGRMDRIGAGSLGCG 19

RESULT 29
US-08-850-910A-34
; Sequence 34, Application US/08850910A
; Patent No. 5948761
; GENERAL INFORMATION:
; APPLICANT: SEILHAMER, J.J.
; APPLICANT: LEWICKI, J.
; APPLICANT: SCARBOROUGH, R.M.
; TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
; TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIURETIC PEPTIDE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER, LLP
; STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
; CITY: Washington
```

STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,910A
FILING DATE: 05-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/477,226
FILING DATE: 08-FEB-1990
APPLICATION NUMBER: 07/299,880
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206,470
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200,383
FILING DATE: 31-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: Murabidge, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 219002025212
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
TELEX:
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-850-910A-34

Query Match 80.9%; Score 55; DB 1; Length 20;
Best Local Similarity 58.8%; Pred. No. 7.4e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFCGXXDRIGXXSXXGC 17
Db 3 CFCGRRLDRIGSLSGLC 19

RESULT 30
US-09-902-517-32
Sequence 32, Application US/09902517
Patent No. 6897030
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Lewicki, John
APPLICANT: Scarborough, Robert M.
TITLE OF INVENTION: IMMUNOASSAYS FOR HUMAN AND CANINE BRAIN
FILE REFERENCE: 219002025213
CURRENT APPLICATION NUMBER: US/09/902,517
FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 09/287,892
FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: 08/850,910
FILING DATE: 1997-05-05
PRIOR APPLICATION NUMBER: 07/477,226
FILING DATE: 1990-02-08
PRIOR APPLICATION NUMBER: 07/299,880
FILING DATE: 1989-01-19
PRIOR APPLICATION NUMBER: 07/206,470
FILING DATE: 1988-06-14
PRIOR APPLICATION NUMBER: 07/200,383
FILING DATE: 1988-05-31

NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 32
LENGTH: 20
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Amino acids encoding pBNP
US-09-902-517-32

Query Match 80.9%; Score 55; DB 2; Length 20;
Best Local Similarity 58.8%; Pred. No. 7.4e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFCGXXDRIGXXSXXGC 17
Db 3 CFCGRMDRIGAGSLGIC 19

RESULT 31
US-09-902-517-34
Sequence 34, Application US/09902517
Patent No. 6897030
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Lewicki, John
APPLICANT: Scarborough, Robert M.
TITLE OF INVENTION: IMMUNOASSAYS FOR HUMAN AND CANINE BRAIN
FILE REFERENCE: 219002025213
CURRENT APPLICATION NUMBER: US/09/902,517
FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 09/287,892
FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: 08/850,910
FILING DATE: 1997-05-05
PRIOR APPLICATION NUMBER: 07/477,226
FILING DATE: 1990-02-08
PRIOR APPLICATION NUMBER: 07/299,880
FILING DATE: 1989-01-19
PRIOR APPLICATION NUMBER: 07/206,470
FILING DATE: 1988-06-14
PRIOR APPLICATION NUMBER: 07/200,383
FILING DATE: 1988-05-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 20
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Amino acids encoding pBNP
US-09-902-517-34

Query Match 80.9%; Score 55; DB 2; Length 20;
Best Local Similarity 58.8%; Pred. No. 7.4e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFCGXXDRIGXXSXXGC 17
Db 3 CFCGRRLDRIGSLSGLC 19

RESULT 32
5212286-30
Patent No. 5212286
APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
PEPTIDE COMPOUNDS
NUMBER OF SEQUENCES: 68
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,795

```

; FILING DATE: 05-JUN-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 766,030
; FILING DATE: 08-MAY-1985
; APPLICATION NUMBER: 602,117
; FILING DATE: 09-APR-1984
; APPLICATION NUMBER: 616,488
; FILING DATE: 01-JUN-1984
; SEQ ID NO:30:
; LENGTH: 20
5212286-30

Query Match          80.9%; Score 55; DB 6; Length 20;
Best Local Similarity 58.8%; Pred. No. 7.4e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17
   ||| ||| ||| |||
Db 4 CFGGRMDRIGAGSGLGC 20

RESULT 33
5212286-51
; Patent No. 5212286
; APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
; PEPTIDE COMPOUNDS
; NUMBER OF SEQUENCES: 68
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/870,795
; FILING DATE: 05-JUN-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 766,030
; FILING DATE: 08-MAY-1985
; APPLICATION NUMBER: 602,117
; FILING DATE: 09-APR-1984
; APPLICATION NUMBER: 616,488
; FILING DATE: 01-JUN-1984
; SEQ ID NO:51:
; LENGTH: 20
5212286-51

Query Match          80.9%; Score 55; DB 6; Length 20;
Best Local Similarity 58.8%; Pred. No. 7.4e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17
   ||| ||| ||| |||
Db 4 CFGGRMDRIGAGSGLGC 20

RESULT 34
US-08-257-446-2
; Sequence 2, Application US/08257446
; Patent No. 5565606
; GENERAL INFORMATION:
; APPLICANT: Briephol, Gerhard
; TITLE OF INVENTION: The Synthesis of Peptide
; TITLE OF INVENTION: Aminoalkylamides and Peptide Hydrazides by the Solid Phase
; TITLE OF INVENTION: Method
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,446
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 783,335
; FILING DATE: 28-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lindeman, Jeffrey A.
; REGISTRATION NUMBER: 34,658
; REFERENCE/DOCKET NUMBER: 02481-0503-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-208-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-257-446-2

Query Match          80.9%; Score 55; DB 1; Length 21;
Best Local Similarity 58.8%; Pred. No. 7.8e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17
   ||| ||| ||| |||
Db 2 CFGGRMDRIGAGSGLGC 18

RESULT 35
US-09-623-548A-483
; Sequence 483, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 483
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-623-548A-483

Query Match          80.9%; Score 55; DB 2; Length 21;
Best Local Similarity 58.8%; Pred. No. 7.8e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17
   ||| ||| ||| |||
```


Db 3 CFGGRIDRIGASGLGC 19

RESULT 36

US-09-657-276-483
; Sequence 483, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 483
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-657-276-483

Query Match 80.9%; Score 55; DB 2; Length 21;

Best Local Similarity 58.8%; Pred. No. 7.8e-05; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17

Db 3 CFGGRIDRIGASGLGC 19

RESULT 37

5212286-41
; Patent No. 5212286
; APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
; PEPTIDE COMPOUNDS
; NUMBER OF SEQUENCES: 68
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/870,795
; FILING DATE: 05-JUN-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 766,030
; FILING DATE: 08-MAY-1985
; APPLICATION NUMBER: 602,117
; FILING DATE: 09-APR-1984
; APPLICATION NUMBER: 616,488
; FILING DATE: 01-JUN-1984
; SEQ ID NO:41
; LENGTH: 21
5212286-41

Query Match 80.9%; Score 55; DB 6; Length 21;

Best Local Similarity 58.8%; Pred. No. 7.8e-05; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17

||| |||| | ||

Db 2 CFGGRIDRIGASGLGC 18

RESULT 38

US-07-754-958-1
; Sequence 1, Application US/07754958
; Patent No. 5336759
; GENERAL INFORMATION:
; APPLICANT: MATSUO, HISAYUKI
; APPLICANT: KANGAWA, KENJI
; APPLICANT: MINAMINO, NAOTO
; TITLE OF INVENTION: A NOVEL BIOLOGICALLY ACTIVE PEPTIDE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/754,958
; FILING DATE: 19910904
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T
; REGISTRATION NUMBER: 56281
; REFERENCE/DOCKET NUMBER: 9437/92322
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO. 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-754-958-1

Query Match 80.9%; Score 55; DB 1; Length 22;

Best Local Similarity 58.8%; Pred. No. 8.2e-05; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17

Db 6 CFGVLDRIAGAFSGLC 22

RESULT 39

US-07-754-958-7
; Sequence 7, Application US/07754958
; Patent No. 5336759
; GENERAL INFORMATION:
; APPLICANT: MATSUO, HISAYUKI
; APPLICANT: KANGAWA, KENJI
; APPLICANT: MINAMINO, NAOTO
; TITLE OF INVENTION: A NOVEL BIOLOGICALLY ACTIVE PEPTIDE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/754,958
FILING DATE: 19910904
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T
REGISTRATION NUMBER: 56281
REFERENCE/DOCKET NUMBER: 9437/92322
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-754-958-7

Query Match 80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSGC 17
DB 6 CFGKLDRIGMSGGCG 22

RESULT 40
US-07-754-947-1
Sequence 1, Application US/07754947
Patent No. 5338830
GENERAL INFORMATION:
APPLICANT: MATSUO, HISAYUKI
APPLICANT: KANGAWA, KENJI
APPLICANT: MINAMINO, NAOTO
TITLE OF INVENTION: A NOVEL BIOLOGICALLY ACTIVE PEPTIDE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1625 L STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/754,947
FILING DATE: 19910904
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 5683/92321
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-754-947-1

Query Match 80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSGC 17
DB 6 CFGVLDRIIGMSGGCG 22

RESULT 41
US-07-754-947-7
Sequence 7, Application US/07754947
Patent No. 5338830
GENERAL INFORMATION:
APPLICANT: MATSUO, HISAYUKI
APPLICANT: KANGAWA, KENJI
APPLICANT: MINAMINO, NAOTO
TITLE OF INVENTION: A NOVEL BIOLOGICALLY ACTIVE PEPTIDE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1625 L STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/754,947
FILING DATE: 19910904
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 5683/92321
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-754-947-7

Query Match 80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSGC 17
DB 6 CFGKLDRIGMSGGCG 22

RESULT 42
US-07-728-221B-2
Sequence 2, Application US/07728221B
Patent No. 5340920
GENERAL INFORMATION:
APPLICANT: Matsuo, Hisayuki
APPLICANT: Kangawa, Kenji
APPLICANT: Minamino, Naoto

;; TITLE OF INVENTION: NOVEL HYSIOLOGICALLY ACTIVE PORCINE
;; TITLE OF INVENTION: PEPTIDE (CNP-53)
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
;; STREET: ELEVENTH FLOOR, 1615 1 STREET, N.W.
;; CITY: WASHINGTON
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20036-5601
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/728,221B
;; FILING DATE: 19910712
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SCOTT, WATSON T.
;; REGISTRATION NUMBER: 26,581
;; REFERENCE/DOCKET NUMBER: WTS/9437/91817/KIK
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 861-3000
;; TELEFAX: (202) 822-0944
;; TELEX: 671 4627 CUSH
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 22 amino acids
;; TYPE: AMINO ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-07-728-221B-2

Query Match 80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
DB 6 CFGKLDRIGSMGLGC 22

RESULT 43
US-07-728-221B-11
; Sequence 11, Application US/07728221B
; Patent No. 5340920
; GENERAL INFORMATION:
; APPLICANT: Matsuo, Hisayuki
; APPLICANT: Kangawa, Kenji
; APPLICANT: Minamino, Naoto
; TITLE OF INVENTION: NOVEL HYSIOLOGICALLY ACTIVE PORCINE
; TITLE OF INVENTION: PEPTIDE (CNP-53)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: ELEVENTH FLOOR, 1615 1 STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/728,221B
; FILING DATE: 19910712
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:

;; NAME: SCOTT, WATSON T.
;; REGISTRATION NUMBER: 26,581
;; REFERENCE/DOCKET NUMBER: WTS/9437/91817/KIK
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 861-3000
;; TELEFAX: (202) 822-0944
;; TELEX: 671 4627 CUSH
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 22 amino acids
;; TYPE: AMINO ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-07-728-221B-11

Query Match 80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
DB 6 CFGKLDRIGSMGLGC 22

RESULT 44
US-07-778-847-3
; Sequence 3, Application US/07778847
; Patent No. 5352770
; GENERAL INFORMATION:
; APPLICANT: MATSUO, HISAYUKI
; TITLE OF INVENTION: PORCINE DERIVED NOVEL PHYSIOLOGICALLY
; TITLE OF INVENTION: ACTIVE PEPTIDE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/778,847
; FILING DATE: 19921220
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: 9437/93819
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3067
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;; US-07-778-847-3

Query Match 80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
DB 6 CFGKLDRIGSMGLGC 22

Db 6 CFGKLKDRIGSMGSLGC 22

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RESULT 45
US-07-828-450-2
; Sequence 2, Application US/07828450
; Patent No. 5434133
; GENERAL INFORMATION:
; APPLICANT: TANAKA, SHOJI
; APPLICANT: MINAMITAKE, YOSHIMARU
; APPLICANT: KITAJIMA, YASUO
; APPLICANT: FURUYA, MAYUMI
; APPLICANT: MATSUO, HISAYUKI
; TITLE OF INVENTION: CNP ANALOG PEPTIDES AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1625 L STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/828,450
; FILING DATE: 19920131
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: 9437/94133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3067
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-07-828-450-2
Query Match 80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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Qy 1 CFGXXXDRIGXXSXXGC 17
Db 6 CFGKLKDRIGSMGSLGC 22

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RESULT 46
US-07-828-450-8
; Sequence 8, Application US/07828450
; Patent No. 5434133
; GENERAL INFORMATION:
; APPLICANT: TANAKA, SHOJI
; APPLICANT: MINAMITAKE, YOSHIMARU
; APPLICANT: KITAJIMA, YASUO
; APPLICANT: FURUYA, MAYUMI
; APPLICANT: MATSUO, HISAYUKI
; TITLE OF INVENTION: CNP ANALOG PEPTIDES AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1625 L STREET, N.W.
; CITY: WASHINGTON
```

```
STATE: D.C.
COUNTRY: USA
ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/828,450
; FILING DATE: 19920131
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: 9437/94133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3067
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-07-828-450-8
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Query Match 80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXXGC 17
Db 6 CFGKLKDRIGSMGSLGC 22

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RESULT 47
US-07-828-450-9
; Sequence 9, Application US/07828450
; Patent No. 5434133
; GENERAL INFORMATION:
; APPLICANT: TANAKA, SHOJI
; APPLICANT: MINAMITAKE, YOSHIMARU
; APPLICANT: KITAJIMA, YASUO
; APPLICANT: FURUYA, MAYUMI
; APPLICANT: MATSUO, HISAYUKI
; TITLE OF INVENTION: CNP ANALOG PEPTIDES AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1625 L STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/828,450
; FILING DATE: 19920131
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: 9437/94133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3067
; TELEFAX: 202-822-0944
```

TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-828-450-9

Query Match 80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CPGXXXDRIGXXSXGC 17
DB 6 CPGLRIDRIGSMGSLGC 22

RESULT 48
US-07-828-450-10
Sequence 10, Application US/07828450
Patent No. 5434133
GENERAL INFORMATION:
APPLICANT: TANAKA, SHOJI
APPLICANT: MINAMITAKE, YOSHIHARU
APPLICANT: KITAJIMA, YASUO
APPLICANT: FURUYA, MAYUMI
APPLICANT: MATSUO, HISAYUKI
TITLE OF INVENTION: CNP ANALOG PEPTIDES AND THEIR USE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1625 L STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/828,450
FILING DATE: 19920131
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 9437/94133
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-828-450-10

Query Match 80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CPGXXXDRIGXXSXGC 17
DB 6 CPGLRIDRIGSMGSLGC 22

RESULT 49
US-07-828-450-11

Sequence 11, Application US/07828450
Patent No. 5434133
GENERAL INFORMATION:
APPLICANT: TANAKA, SHOJI
APPLICANT: MINAMITAKE, YOSHIHARU
APPLICANT: KITAJIMA, YASUO
APPLICANT: FURUYA, MAYUMI
APPLICANT: MATSUO, HISAYUKI
TITLE OF INVENTION: CNP ANALOG PEPTIDES AND THEIR USE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1625 L STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/828,450
FILING DATE: 19920131
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 9437/94133
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-828-450-11

Query Match 80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CPGXXXDRIGXXSXGC 17
DB 6 CPGLRIDRIGSMGSLGC 22

RESULT 50
US-07-828-450-12
Sequence 12, Application US/07828450
Patent No. 5434133
GENERAL INFORMATION:
APPLICANT: TANAKA, SHOJI
APPLICANT: MINAMITAKE, YOSHIHARU
APPLICANT: KITAJIMA, YASUO
APPLICANT: FURUYA, MAYUMI
APPLICANT: MATSUO, HISAYUKI
TITLE OF INVENTION: CNP ANALOG PEPTIDES AND THEIR USE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1625 L STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/828,450
FILING DATE: 19920131
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 9437/94133
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-828-450-12

Query Match 80.9%; Score 55; DB 1; Length 22;
Best Local Similarity 58.8%; Pred. No. 8.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXXXGC 17
Db 6 CFGLKDRIGSQSGUGC 22

Search completed: January 26, 2006, 14:46:01
Job time : 27 secs

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OM protein - protein search, using sw model

Run on: January 26, 2006, 14:42:13 ; Search time 61 Seconds
(without alignments)
116.444 Million cell updates/sec

Title: US-10-664-605-5

Perfect score: 68
Sequence: 1 CFGXXDRIGKXXKGC 17

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA Main:

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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBSCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBSCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	56	82.4	17	4	US-10-664-605-40
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4	56	82.4	17	4	US-10-664-605-58
5	56	82.4	17	4	US-10-664-605-63
6	56	82.4	17	4	US-10-664-605-68
7	56	82.4	20	6	US-11-066-697-469
8	56	82.4	21	6	US-11-066-697-470
9	56	82.4	24	3	US-09-752-724-5
10	56	82.4	24	6	US-11-066-697-468
11	56	82.4	24	6	US-11-066-697-471
12	56	82.4	30	6	US-11-066-697-472
13	55	80.9	17	3	US-09-902-517-15
14	55	80.9	17	3	US-09-027-777B-1
15	55	80.9	17	4	US-10-327-514-17
16	55	80.9	17	4	US-10-327-514-18
17	55	80.9	17	4	US-10-327-514-19
18	55	80.9	17	4	US-10-402-021-15
19	55	80.9	17	4	US-10-664-605-2
20	55	80.9	17	4	US-10-664-605-41
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22	55	80.9	17	4	US-10-664-605-43
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24	55	80.9	17	4	US-10-664-605-46
25	55	80.9	17	4	US-10-664-605-47
26	55	80.9	17	4	US-10-664-605-54
27	55	80.9	17	4	US-10-664-605-56

28	55	80.9	17	4	US-10-664-605-59	Sequence 59, App1
29	55	80.9	17	4	US-10-664-605-60	Sequence 60, App1
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31	55	80.9	17	4	US-10-664-605-62	Sequence 62, App1
32	55	80.9	17	4	US-10-664-605-64	Sequence 64, App1
33	55	80.9	17	4	US-10-664-605-66	Sequence 66, App1
34	55	80.9	17	4	US-10-664-605-67	Sequence 67, App1
35	55	80.9	17	4	US-10-664-605-69	Sequence 69, App1
36	55	80.9	17	5	US-10-499-762-17	Sequence 17, App1
37	55	80.9	17	5	US-10-499-762-18	Sequence 18, App1
38	55	80.9	17	5	US-10-499-762-19	Sequence 19, App1
39	55	80.9	17	6	US-11-066-697-474	Sequence 474, App
40	55	80.9	20	3	US-09-902-517-32	Sequence 32, App1
41	55	80.9	20	4	US-10-402-021-32	Sequence 34, App1
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44	55	80.9	21	6	US-11-066-697-483	Sequence 483, App
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48	55	80.9	22	3	US-09-752-724-11	Sequence 11, App1
49	55	80.9	22	3	US-09-466-268B-9	Sequence 9, App1
50	55	80.9	22	3	US-09-912-425-3	Sequence 9, App1
51	55	80.9	22	4	US-10-106-806-8	Sequence 8, App1
52	55	80.9	22	4	US-10-106-806-9	Sequence 9, App1
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54	55	80.9	22	4	US-10-723-933-77	Sequence 77, App1
55	55	80.9	22	5	US-10-471-348-13	Sequence 13, App1
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57	55	80.9	22	5	US-10-471-348-23	Sequence 23, App1
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59	55	80.9	22	5	US-10-947-720-9	Sequence 9, App1
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62	55	80.9	22	6	US-11-040-810-17	Sequence 17, App1
63	55	80.9	22	6	US-11-040-810-23	Sequence 23, App1
64	55	80.9	22	6	US-11-066-697-475	Sequence 475, App
65	55	80.9	22	6	US-11-066-697-508	Sequence 508, App
66	55	80.9	22	6	US-11-066-697-517	Sequence 517, App
67	55	80.9	22	6	US-11-066-697-518	Sequence 518, App
68	55	80.9	23	6	US-11-066-697-481	Sequence 481, App
69	55	80.9	23	6	US-11-066-697-484	Sequence 484, App
70	55	80.9	23	6	US-11-066-697-524	Sequence 524, App
71	55	80.9	24	5	US-10-471-348-15	Sequence 15, App1
72	55	80.9	24	5	US-10-471-348-16	Sequence 16, App1
73	55	80.9	24	6	US-11-040-810-16	Sequence 16, App1
74	55	80.9	24	6	US-11-066-697-473	Sequence 15, App1
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76	55	80.9	24	6	US-11-066-697-487	Sequence 487, App
77	55	80.9	24	6	US-11-066-697-502	Sequence 502, App
78	55	80.9	24	6	US-11-066-697-505	Sequence 505, App
79	55	80.9	25	3	US-09-902-517-2	Sequence 2, App1
80	55	80.9	25	4	US-10-402-021-2	Sequence 2, App1
81	55	80.9	25	4	US-10-156-557-16	Sequence 16, App1
82	55	80.9	25	6	US-11-066-697-480	Sequence 480, App
83	55	80.9	25	6	US-11-066-697-488	Sequence 488, App
84	55	80.9	26	3	US-09-902-517-3	Sequence 3, App1
85	55	80.9	26	4	US-10-402-021-3	Sequence 3, App1
86	55	80.9	26	4	US-10-723-933-35	Sequence 35, App1
87	55	80.9	26	4	US-10-723-933-35	Sequence 35, App1
88	55	80.9	26	4	US-11-066-697-478	Sequence 478, App
89	55	80.9	26	6	US-11-066-697-479	Sequence 479, App
90	55	80.9	26	6	US-11-066-697-511	Sequence 511, App
91	55	80.9	26	6	US-11-066-697-511	Sequence 511, App
92	55	80.9	27	4	US-10-197-994-142	Sequence 142, App1
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94	55	80.9	27	4	US-10-360-101-25	Sequence 25, App1
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98	55	80.9	27	6	US-11-066-697-501	Sequence 501, App
99	55	80.9	27	6	US-11-066-697-523	Sequence 523, App
100	55	80.9	28	3	US-09-752-724-1	Sequence 1, App1

101	55	80.9	28	3	US-09-752-724-2	Sequence 2, Appl.i	174	55	80.9	103	3	US-09-912-425-2	Sequence 2, Appl.i
102	55	80.9	28	3	US-09-466-268B-5	Sequence 5, Appl.i	175	55	80.9	106	3	US-09-902-517-30	Sequence 30, Appl
103	55	80.9	28	4	US-10-106-806-5	Sequence 5, Appl.i	176	55	80.9	106	3	US-10-402-021-30	Sequence 30, Appl
104	55	80.9	28	4	US-10-197-954-14	Sequence 14, Appl	177	55	80.9	126	3	US-09-912-425-1	Sequence 1, Appl.i
105	55	80.9	28	4	US-10-279-061-14	Sequence 1, Appl.i	178	55	80.9	126	4	US-10-419-059-3	Sequence 3, Appl.i
106	55	80.9	28	4	US-10-279-061-76	Sequence 76, Appl	179	55	80.9	126	4	US-10-419-059-5	Sequence 5, Appl.i
107	55	80.9	28	4	US-10-343-654-16	Sequence 16, Appl	180	55	80.9	126	4	US-10-645-874-3	Sequence 3, Appl.i
108	55	80.9	28	4	US-10-360-101-84	Sequence 84, Appl	181	55	80.9	126	4	US-10-645-874-5	Sequence 5, Appl.i
109	55	80.9	28	4	US-10-723-933-78	Sequence 78, Appl	182	55	80.9	126	5	US-10-827-919-3	Sequence 3, Appl.i
110	55	80.9	28	5	US-10-471-348-1	Sequence 1, Appl.i	183	55	80.9	126	5	US-10-827-919-5	Sequence 5, Appl.i
111	55	80.9	28	5	US-10-471-348-2	Sequence 2, Appl.i	184	55	80.9	126	5	US-10-737-318-35	Sequence 35, Appl
112	55	80.9	28	5	US-10-471-348-3	Sequence 3, Appl.i	185	55	80.9	126	5	US-10-737-318-38	Sequence 38, Appl
113	55	80.9	28	5	US-10-471-348-4	Sequence 4, Appl.i	186	55	80.9	131	3	US-09-902-517-39	Sequence 39, Appl
114	55	80.9	28	5	US-10-471-348-7	Sequence 7, Appl.i	187	55	80.9	131	3	US-09-902-517-41	Sequence 41, Appl
115	55	80.9	28	5	US-10-471-348-12	Sequence 12, Appl	188	55	80.9	131	3	US-09-902-517-43	Sequence 43, Appl
116	55	80.9	28	5	US-10-718-071-20	Sequence 20, Appl	189	55	80.9	131	3	US-09-902-517-46	Sequence 46, Appl
117	55	80.9	28	5	US-10-718-071-41	Sequence 41, Appl	190	55	80.9	131	4	US-10-279-061-88	Sequence 88, Appl
118	55	80.9	28	5	US-10-760-085-14	Sequence 14, Appl	191	55	80.9	131	4	US-10-402-021-39	Sequence 39, Appl
119	55	80.9	28	5	US-10-947-730-5	Sequence 5, Appl.i	192	55	80.9	131	4	US-10-402-021-41	Sequence 41, Appl
120	55	80.9	28	5	US-10-989-397-1	Sequence 1, Appl.i	193	55	80.9	131	4	US-10-402-021-43	Sequence 43, Appl
121	55	80.9	28	5	US-10-775-204-2207	Sequence 2207, Ap	194	55	80.9	131	4	US-10-402-021-46	Sequence 46, Appl
122	55	80.9	28	6	US-11-040-810-1	Sequence 1, Appl.i	195	55	80.9	132	3	US-09-902-517-47	Sequence 47, Appl
123	55	80.9	28	6	US-11-040-810-2	Sequence 2, Appl.i	196	55	80.9	132	4	US-10-402-021-47	Sequence 47, Appl
124	55	80.9	28	6	US-11-040-810-3	Sequence 3, Appl.i	197	55	80.9	151	4	US-10-419-059-4	Sequence 4, Appl.i
125	55	80.9	28	6	US-11-040-810-4	Sequence 4, Appl.i	198	55	80.9	151	4	US-10-645-874-4	Sequence 4, Appl.i
126	55	80.9	28	6	US-11-040-810-7	Sequence 7, Appl.i	199	55	80.9	151	5	US-10-982-919-4	Sequence 4, Appl
127	55	80.9	28	6	US-11-040-810-12	Sequence 12, Appl	200	55	80.9	152	5	US-10-982-919-16	Sequence 16, Appl
128	55	80.9	28	6	US-11-066-697-476	Sequence 476, App	201	55	80.9	153	4	US-10-201-288-17	Sequence 17, Appl
129	55	80.9	28	6	US-11-066-697-486	Sequence 486, App	202	55	80.9	153	5	US-10-919-325-6	Sequence 6, Appl.i
130	55	80.9	28	6	US-11-066-697-495	Sequence 495, App	203	55	80.9	157	5	US-10-982-514-17	Sequence 17, Appl
131	55	80.9	29	3	US-09-772-607-3	Sequence 3, Appl.i	204	55	80.9	161	3	US-09-864-408A-4402	Sequence 4402, Ap
132	55	80.9	29	3	US-09-772-607-9	Sequence 9, Appl.i	205	55	80.9	196	4	US-10-201-288-2	Sequence 2, Appl.i
133	55	80.9	29	3	US-09-752-724-8	Sequence 8, Appl.i	206	55	80.9	196	5	US-10-919-325-2	Sequence 2, Appl.i
134	55	80.9	29	4	US-10-664-605-3	Sequence 3, Appl.i	207	55	80.9	265	5	US-10-471-931-2	Sequence 2, Appl.i
135	55	80.9	29	5	US-10-471-348-5	Sequence 5, Appl.i	208	54	79.4	17	4	US-10-664-605-5	Sequence 5, Appl.i
136	55	80.9	29	6	US-11-040-810-5	Sequence 5, Appl.i	209	54	79.4	17	4	US-10-664-605-52	Sequence 52, Appl
137	55	80.9	29	6	US-11-066-697-465	Sequence 465, App	210	54	79.4	17	4	US-10-664-605-55	Sequence 55, Appl
138	55	80.9	31	3	US-09-964-201A-22	Sequence 22, Appl	211	54	79.4	17	4	US-10-664-605-57	Sequence 57, Appl
139	55	80.9	31	4	US-10-681-389-22	Sequence 22, Appl	212	54	79.4	17	4	US-10-664-605-65	Sequence 65, Appl
140	55	80.9	31	4	US-10-681-388-22	Sequence 22, Appl	213	54	79.4	28	5	US-10-471-348-6	Sequence 6, Appl.i
141	55	80.9	32	3	US-09-752-724-6	Sequence 6, Appl.i	214	54	79.4	28	6	US-11-040-810-6	Sequence 6, Appl.i
142	55	80.9	32	3	US-09-027-777B-5	Sequence 5, Appl.i	215	53	77.9	17	4	US-10-664-605-51	Sequence 51, Appl
143	55	80.9	32	3	US-09-027-777B-10	Sequence 10, Appl	216	52	76.5	17	4	US-10-664-605-49	Sequence 49, Appl
144	55	80.9	32	3	US-09-027-777B-11	Sequence 11, Appl	217	51	75.0	17	4	US-10-664-605-35	Sequence 35, Appl
145	55	80.9	32	4	US-10-723-933-74	Sequence 74, Appl	218	51	75.0	17	4	US-10-664-605-50	Sequence 50, Appl
146	55	80.9	32	4	US-10-723-933-75	Sequence 75, Appl	219	50	73.5	17	4	US-10-664-605-9	Sequence 9, Appl.i
147	55	80.9	32	4	US-10-723-933-137	Sequence 137, App	220	50	73.5	17	4	US-10-664-605-31	Sequence 31, Appl
148	55	80.9	32	5	US-10-471-348-8	Sequence 8, Appl.i	221	50	73.5	17	4	US-10-664-605-48	Sequence 48, Appl
149	55	80.9	32	5	US-10-471-348-9	Sequence 9, Appl.i	222	50	73.5	17	4	US-10-664-605-48	Sequence 48, Appl
150	55	80.9	32	5	US-10-471-348-10	Sequence 10, Appl	223	50	73.5	17	4	US-10-664-605-53	Sequence 53, Appl
151	55	80.9	32	5	US-10-989-397-4	Sequence 4, Appl.i	224	50	73.5	17	4	US-10-723-933-1	Sequence 1, Appl.i
152	55	80.9	32	5	US-10-775-204-2203	Sequence 2203, Ap	225	50	73.5	17	4	US-10-723-933-79	Sequence 79, Appl
153	55	80.9	32	6	US-11-040-810-8	Sequence 8, Appl.i	226	50	73.5	17	4	US-10-723-933-128	Sequence 128, App
154	55	80.9	32	6	US-11-040-810-9	Sequence 9, Appl.i	227	50	73.5	17	4	US-10-723-933-132	Sequence 132, App
155	55	80.9	32	6	US-11-040-810-10	Sequence 10, Appl	228	50	73.5	17	5	US-10-737-290-172	Sequence 172, App
156	55	80.9	32	6	US-11-066-697-490	Sequence 490, App	229	50	73.5	18	4	US-10-723-933-21	Sequence 21, Appl
157	55	80.9	32	6	US-11-066-697-504	Sequence 504, App	230	50	73.5	18	4	US-10-723-933-129	Sequence 129, App
158	55	80.9	32	6	US-11-066-697-507	Sequence 507, App	231	50	73.5	18	5	US-10-471-348-41	Sequence 41, Appl
159	55	80.9	32	6	US-11-066-697-512	Sequence 512, App	232	50	73.5	18	5	US-10-471-348-44	Sequence 44, Appl
160	55	80.9	32	6	US-11-066-697-513	Sequence 513, App	233	50	73.5	18	6	US-11-040-810-41	Sequence 41, Appl
161	55	80.9	32	6	US-09-466-268B-2	Sequence 2, Appl.i	234	50	73.5	18	6	US-11-040-810-44	Sequence 44, Appl
162	55	80.9	37	3	US-09-027-777B-4	Sequence 4, Appl.i	235	50	73.5	23	4	US-10-723-933-84	Sequence 84, Appl
163	55	80.9	37	4	US-10-106-806-2	Sequence 2, Appl.i	236	50	73.5	23	4	US-10-723-933-110	Sequence 130, App
164	55	80.9	37	4	US-10-947-730-2	Sequence 2, Appl.i	237	50	73.5	23	5	US-10-471-348-28	Sequence 28, Appl
165	55	80.9	41	3	US-09-902-517-50	Sequence 50, Appl	238	50	73.5	23	5	US-10-471-348-31	Sequence 31, Appl
166	55	80.9	42	4	US-10-279-061-84	Sequence 84, Appl	239	50	73.5	23	6	US-11-040-810-28	Sequence 28, Appl
167	55	80.9	45	3	US-09-752-724-7	Sequence 7, Appl.i	240	50	73.5	23	6	US-11-040-810-31	Sequence 31, Appl
168	55	80.9	45	6	US-11-066-697-510	Sequence 510, App	241	50	73.5	24	4	US-10-723-933-127	Sequence 127, App
169	55	80.9	45	6	US-11-066-697-514	Sequence 514, App	242	50	73.5	24	5	US-10-471-348-30	Sequence 30, Appl
170	55	80.9	53	4	US-10-360-101-87	Sequence 87, Appl	243	50	73.5	24	5	US-10-471-348-33	Sequence 33, Appl
171	55	80.9	53	6	US-11-066-697-519	Sequence 519, App	244	50	73.5	24	6	US-11-040-810-30	Sequence 30, Appl
172	55	80.9	53	6	US-11-066-697-520	Sequence 520, App	245	50	73.5	24	6	US-11-040-810-33	Sequence 33, Appl
173	55	80.9	56	6	US-11-066-697-489	Sequence 489, App	246	50	73.5	25	4	US-10-723-933-18	Sequence 18, Appl

247	50	73.5	25	4	US-10-723-933-126	Sequence 126, App	320	50	73.5	35	6	US-11-066-697-506	Sequence 506, App
248	50	73.5	25	5	US-10-471-348-22	Sequence 22, Appl	321	50	73.5	36	4	US-10-723-933-80	Sequence 80, Appl
249	50	73.5	25	5	US-10-471-348-24	Sequence 24, Appl	322	50	73.5	37	4	US-10-723-933-117	Sequence 117, App
250	50	73.5	25	5	US-10-471-348-25	Sequence 25, Appl	323	50	73.5	37	4	US-09-466-268B-1	Sequence 1, Appl1
251	50	73.5	25	5	US-10-771-348-26	Sequence 26, Appl	324	50	73.5	41	3	US-10-106-806-1	Sequence 1, Appl1
252	50	73.5	25	6	US-11-040-810-22	Sequence 22, Appl	325	50	73.5	41	4	US-10-947-730-1	Sequence 1, Appl1
253	50	73.5	25	6	US-11-040-810-24	Sequence 24, Appl	326	50	73.5	41	5	US-10-419-059-1	Sequence 1, Appl1
254	50	73.5	25	6	US-11-040-810-25	Sequence 25, Appl	327	50	73.5	108	4	US-10-300-733-1	Sequence 1, Appl1
255	50	73.5	25	6	US-11-040-810-26	Sequence 26, Appl	328	50	73.5	108	4	US-10-359-051-1	Sequence 1, Appl1
256	50	73.5	26	3	US-09-902-517-1	Sequence 1, Appl1	329	50	73.5	108	4	US-10-645-874-1	Sequence 1, Appl1
257	50	73.5	26	4	US-10-106-806-7	Sequence 7, Appl1	330	50	73.5	108	5	US-10-714-078-1	Sequence 1, Appl1
258	50	73.5	26	4	US-10-402-021-1	Sequence 1, Appl1	331	50	73.5	108	5	US-10-603-891-1	Sequence 1, Appl1
259	50	73.5	26	4	US-10-723-933-107	Sequence 107, App	332	50	73.5	108	5	US-10-827-919-1	Sequence 1, Appl1
260	50	73.5	26	4	US-10-723-933-124	Sequence 124, App	333	50	73.5	108	5	US-10-938-276-1	Sequence 1, Appl1
261	50	73.5	26	5	US-10-471-348-27	Sequence 27, Appl	334	50	73.5	108	5	US-10-952-275-1	Sequence 1, Appl1
262	50	73.5	26	5	US-10-947-730-7	Sequence 7, Appl1	335	50	73.5	134	3	US-09-902-517-45	Sequence 45, Appl
263	50	73.5	26	6	US-11-040-810-27	Sequence 27, Appl	336	50	73.5	134	3	US-09-902-517-48	Sequence 48, Appl
264	50	73.5	29	4	US-10-723-933-106	Sequence 106, App	337	50	73.5	134	3	US-09-508-435-2	Sequence 2, Appl1
265	50	73.5	29	4	US-10-723-933-116	Sequence 116, App	338	50	73.5	134	4	US-10-419-059-2	Sequence 2, Appl1
266	50	73.5	29	4	US-10-723-933-123	Sequence 123, App	339	50	73.5	134	4	US-10-402-021-45	Sequence 45, Appl
267	50	73.5	32	3	US-09-752-724-4	Sequence 4, Appl1	340	50	73.5	134	4	US-10-402-021-48	Sequence 48, Appl
268	50	73.5	32	3	US-09-466-268B-6	Sequence 6, Appl1	341	50	73.5	134	4	US-10-645-874-2	Sequence 22, Appl
269	50	73.5	32	3	US-09-902-517-49	Sequence 49, Appl1	342	50	73.5	134	4	US-10-714-078-2	Sequence 2, Appl1
270	50	73.5	32	4	US-10-106-806-6	Sequence 6, Appl1	343	50	73.5	134	5	US-10-723-933-22	Sequence 2, Appl1
271	50	73.5	32	4	US-10-197-954-24	Sequence 24, Appl	344	50	73.5	134	5	US-10-603-891-2	Sequence 2, Appl1
272	50	73.5	32	4	US-10-402-021-49	Sequence 49, Appl	345	50	73.5	134	5	US-10-827-919-2	Sequence 2, Appl1
273	50	73.5	32	4	US-10-664-605-4	Sequence 4, Appl1	346	50	73.5	134	5	US-10-952-275-2	Sequence 2, Appl1
274	50	73.5	32	4	US-10-723-933-33	Sequence 33, Appl	347	50	73.5	134	5	US-10-775-204-1277	Sequence 1277, Ap
275	50	73.5	32	4	US-10-723-933-53	Sequence 53, Appl	348	50	73.5	195	4	US-10-723-933-115	Sequence 115, App
276	50	73.5	32	4	US-10-723-933-73	Sequence 73, Appl	349	50	73.5	641	5	US-10-775-204-1634	Sequence 1634, Ap
277	50	73.5	32	4	US-10-723-933-82	Sequence 82, Appl	350	50	73.5	179	5	US-10-775-204-175	Sequence 1275, Ap
278	50	73.5	32	4	US-10-723-933-83	Sequence 83, Appl	351	49	72.1	17	4	US-10-664-605-8	Sequence 8, Appl1
279	50	73.5	32	4	US-10-723-933-110	Sequence 110, App	352	49	72.1	17	4	US-10-664-605-28	Sequence 28, Appl
280	50	73.5	32	4	US-10-723-933-111	Sequence 111, App	353	49	72.1	17	4	US-10-664-605-29	Sequence 29, Appl
281	50	73.5	32	4	US-10-723-933-111	Sequence 111, App	354	49	72.1	17	4	US-10-664-605-30	Sequence 30, Appl
282	50	73.5	32	5	US-10-818-246-5	Sequence 5, Appl1	355	49	72.1	17	4	US-10-664-605-35	Sequence 36, Appl
283	50	73.5	32	5	US-10-471-348-21	Sequence 21, Appl	356	49	72.1	17	4	US-10-664-605-70	Sequence 70, Appl
284	50	73.5	32	5	US-10-471-348-45	Sequence 45, Appl	357	49	72.1	32	5	US-10-471-348-57	Sequence 57, Appl
285	50	73.5	32	5	US-10-471-348-45	Sequence 45, Appl	358	49	72.1	32	6	US-11-040-810-57	Sequence 57, Appl
286	50	73.5	32	5	US-10-471-348-48	Sequence 48, Appl	359	48	70.6	17	3	US-09-902-517-5	Sequence 5, Appl1
287	50	73.5	32	5	US-10-471-348-49	Sequence 49, Appl	360	48	70.6	17	4	US-10-402-021-5	Sequence 5, Appl1
288	50	73.5	32	5	US-10-471-348-51	Sequence 51, Appl	361	48	70.6	17	4	US-10-664-605-25	Sequence 25, Appl
289	50	73.5	32	5	US-10-471-348-52	Sequence 52, Appl	362	48	70.6	17	4	US-10-664-605-26	Sequence 26, Appl
290	50	73.5	32	5	US-10-471-348-54	Sequence 54, Appl	363	48	70.6	17	4	US-10-664-605-32	Sequence 32, Appl
291	50	73.5	32	5	US-10-471-348-56	Sequence 56, Appl	364	48	70.6	17	4	US-10-664-605-33	Sequence 33, Appl
292	50	73.5	32	5	US-10-760-085-24	Sequence 24, Appl	365	48	70.6	17	4	US-10-664-605-71	Sequence 71, Appl
293	50	73.5	32	5	US-10-947-730-6	Sequence 6, Appl1	366	48	70.6	23	4	US-10-106-806-11	Sequence 11, Appl
294	50	73.5	32	5	US-10-989-397-2	Sequence 2, Appl1	367	48	70.6	23	5	US-10-947-730-11	Sequence 11, Appl
295	50	73.5	32	5	US-10-775-204-1802	Sequence 1802, Ap	368	48	70.6	28	5	US-10-471-348-19	Sequence 19, Appl
296	50	73.5	32	6	US-11-040-810-21	Sequence 21, Appl	369	48	70.6	28	5	US-10-471-348-19	Sequence 19, Appl
297	50	73.5	32	6	US-11-040-810-45	Sequence 45, Appl	370	48	70.6	28	5	US-10-471-348-20	Sequence 20, Appl
298	50	73.5	32	6	US-11-040-810-46	Sequence 46, Appl	371	48	70.6	28	6	US-11-040-810-11	Sequence 11, Appl
299	50	73.5	32	6	US-11-040-810-48	Sequence 48, Appl	372	48	70.6	28	6	US-11-040-810-19	Sequence 19, Appl
300	50	73.5	32	6	US-11-040-810-49	Sequence 49, Appl	373	48	70.6	28	6	US-11-040-810-20	Sequence 20, Appl
301	50	73.5	32	6	US-11-040-810-51	Sequence 51, Appl	374	48	70.6	33	6	US-11-066-697-515	Sequence 515, App
302	50	73.5	32	6	US-11-040-810-52	Sequence 52, Appl	375	48	70.6	38	3	US-09-466-268B-10	Sequence 10, Appl
303	50	73.5	32	6	US-11-040-810-54	Sequence 54, Appl	376	48	70.6	38	4	US-10-106-806-10	Sequence 10, Appl
304	50	73.5	32	6	US-11-040-810-56	Sequence 56, Appl	377	48	70.6	38	4	US-10-664-605-38	Sequence 38, Appl
305	50	73.5	32	6	US-11-066-697-509	Sequence 509, App	378	48	70.6	38	4	US-10-723-933-76	Sequence 76, Appl
306	50	73.5	33	6	US-11-066-697-516	Sequence 516, App	379	47	69.1	38	5	US-10-947-730-10	Sequence 10, Appl
307	50	73.5	33	6	US-09-942-709-1	Sequence 1, Appl1	380	47	69.1	17	4	US-10-664-605-6	Sequence 6, Appl1
308	50	73.5	33	4	US-10-723-933-5	Sequence 5, Appl1	381	47	69.1	17	4	US-10-664-605-7	Sequence 7, Appl1
309	50	73.5	33	4	US-10-723-933-108	Sequence 108, App	382	47	69.1	17	4	US-10-664-605-34	Sequence 34, Appl
310	50	73.5	33	4	US-10-723-933-112	Sequence 112, App	383	46	67.6	17	4	US-10-664-605-39	Sequence 39, Appl
311	50	73.5	33	5	US-10-697-886-1	Sequence 1, Appl1	384	46	67.6	21	3	US-09-466-268B-8	Sequence 8, Appl1
312	50	73.5	33	5	US-10-471-348-47	Sequence 47, Appl	385	46	67.6	22	5	US-10-471-348-18	Sequence 18, Appl
313	50	73.5	33	5	US-10-471-348-50	Sequence 50, Appl	386	46	67.6	22	5	US-10-471-348-18	Sequence 18, Appl
314	50	73.5	33	5	US-10-471-348-53	Sequence 53, Appl	387	46	67.6	22	6	US-11-040-810-18	Sequence 18, Appl
315	50	73.5	33	5	US-10-471-348-55	Sequence 55, Appl	388	46	67.6	22	6	US-11-040-810-18	Sequence 18, Appl
316	50	73.5	33	6	US-11-040-810-47	Sequence 47, Appl	389	46	67.6	85	4	US-10-425-115-548455	Sequence 348455, Sequence 2, Appl1
317	50	73.5	33	6	US-11-040-810-50	Sequence 50, Appl	390	43	63.2	17	4	US-10-723-933-2	Sequence 2, Appl1
318	50	73.5	33	6	US-11-040-810-53	Sequence 53, Appl	391	43	63.2	17	4	US-10-723-933-109	Sequence 109, App
319	50	73.5	33	6	US-11-040-810-55	Sequence 55, Appl	392	43	63.2	23	5	US-10-471-348-34	Sequence 34, Appl

333	43	63.2	23	5	US-10-471-348-35	Sequence 35, Appl	466	33	48.5	562	4	US-10-437-963-157091	Sequence 157091,
334	43	63.2	23	6	US-11-040-810-34	Sequence 34, Appl	467	33	48.5	781	4	US-10-437-963-16775	Sequence 16775,
335	43	63.2	23	6	US-11-040-810-35	Sequence 35, Appl	468	32	47.1	17	5	US-10-471-348-40	Sequence 40, Appl
336	43	63.2	24	5	US-10-471-348-36	Sequence 36, Appl	469	32	47.1	17	5	US-10-471-348-43	Sequence 43, Appl
337	43	63.2	24	6	US-11-040-810-36	Sequence 36, Appl	470	32	47.1	17	6	US-11-040-810-40	Sequence 40, Appl
338	43	63.2	26	4	US-10-723-933-113	Sequence 113, Appl	471	32	47.1	87	3	US-11-040-810-43	Sequence 43, Appl
339	43	63.2	32	5	US-10-471-348-37	Sequence 37, Appl	472	32	47.1	91	3	US-09-764-891-2746	Sequence 2746, Ap
400	43	63.2	32	6	US-11-040-810-37	Sequence 37, Appl	473	32	47.1	91	4	US-10-630-590-203	Sequence 203, App
401	43	63.2	33	6	US-10-471-348-38	Sequence 38, Appl	474	32	47.1	91	4	US-10-789-102-302	Sequence 302, App
402	43	63.2	33	6	US-11-040-810-38	Sequence 38, Appl	475	32	47.1	91	6	US-11-021-949-332	Sequence 332, App
403	43	63.2	37	6	US-10-723-933-136	Sequence 136, Appl	476	32	47.1	91	6	US-10-938-249-284	Sequence 229, App
404	42	61.8	14	4	US-10-664-605-14	Sequence 14, Appl	477	32	47.1	93	5	US-10-767-701-51260	Sequence 51260, A
405	42	61.8	14	4	US-10-664-605-15	Sequence 15, Appl	478	32	47.1	175	4	US-10-425-115-220696	Sequence 220696,
406	41	60.3	17	5	US-10-471-348-39	Sequence 39, Appl	479	32	47.1	178	4	US-10-425-115-220696	Sequence 220696,
407	41	60.3	17	5	US-10-471-348-42	Sequence 42, Appl	480	32	47.1	223	4	US-10-425-115-217242	Sequence 217242,
408	41	60.3	17	6	US-11-040-810-39	Sequence 39, Appl	481	32	47.1	317	4	US-10-282-112A-19359	Sequence 49359, A
409	41	60.3	17	6	US-11-040-810-42	Sequence 42, Appl	482	32	47.1	321	4	US-10-306-762-209	Sequence 209, App
410	41	60.3	23	5	US-10-471-348-29	Sequence 29, Appl	483	32	47.1	323	4	US-10-306-762-216	Sequence 216, App
411	41	60.3	23	5	US-10-471-348-32	Sequence 32, Appl	484	32	47.1	355	5	US-10-739-930-9926	Sequence 9926, Ap
412	41	60.3	23	6	US-11-040-810-29	Sequence 29, Appl	485	32	47.1	442	5	US-10-732-923-23732	Sequence 23732, A
413	41	60.3	23	6	US-11-040-810-32	Sequence 32, Appl	486	32	47.1	442	5	US-10-732-923-23762	Sequence 23762, A
414	41	60.3	25	3	US-11-040-810-32	Sequence 32, Appl	487	32	47.1	444	5	US-10-732-923-11220	Sequence 11220, A
415	41	60.3	28	4	US-09-466-268B-7	Sequence 7, Appl1	488	32	47.1	445	5	US-10-732-923-23745	Sequence 23745, A
416	41	60.3	32	4	US-10-360-101-86	Sequence 86, Appl	489	32	47.1	459	4	US-10-369-493-18259	Sequence 18259, A
417	40.5	59.6	42	4	US-10-279-061-74	Sequence 74, Appl	490	32	47.1	459	5	US-10-732-923-11215	Sequence 11215, A
418	40	58.8	17	4	US-10-664-605-27	Sequence 27, Appl	491	32	47.1	463	4	US-10-311-765-2	Sequence 2, Appl1
419	40	58.8	17	4	US-11-066-697-496	Sequence 496, App	492	32	47.1	463	4	US-10-408-766A-1522	Sequence 1522, Ap
420	39	57.4	11	6	US-10-664-605-22	Sequence 22, Appl	493	32	47.1	488	5	US-10-732-923-23757	Sequence 23757, A
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422	39	57.4	13	4	US-10-664-605-16	Sequence 16, Appl	495	32	47.1	514	3	US-09-987-701-12	Sequence 12, Appl
423	39	57.4	13	4	US-10-664-605-17	Sequence 17, Appl	496	32	47.1	514	5	US-10-631-467-765	Sequence 765, App
424	39	57.4	13	4	US-10-664-605-18	Sequence 18, Appl	497	32	47.1	514	5	US-10-631-467-765	Sequence 1515, Ap
425	39	57.4	13	4	US-10-664-605-19	Sequence 19, Appl	498	32	47.1	524	4	US-10-437-963-159034	Sequence 159034,
426	39	57.4	15	6	US-11-066-697-493	Sequence 493, App	499	32	47.1	544	5	US-10-732-923-11300	Sequence 11300, A
427	39	57.4	17	4	US-10-664-605-24	Sequence 24, Appl	500	32	47.1	544	5	US-10-437-963-192947	Sequence 192947,
428	39	57.4	22	3	US-09-466-268B-11	Sequence 11, Appl	501	32	47.1	552	4	US-10-282-112A-09450	Sequence 49450, A
429	38	55.9	28	4	US-10-723-933-41	Sequence 41, Appl	502	32	47.1	552	4	US-10-282-112A-05061	Sequence 50601, A
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431	37	54.4	21	6	US-11-066-697-494	Sequence 494, App	504	32	47.1	559	4	US-10-343-253A-7	Sequence 7, Appl1
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433	35	51.5	51	5	US-10-156-761-9568	Sequence 9568, Ap	506	32	47.1	576	6	US-10-275-505-5	Sequence 5, Appl1
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435	35	51.5	2110	5	US-10-732-923-20533	Sequence 20533, A	508	32	47.1	731	4	US-10-275-107-52	Sequence 107, Appl
436	35	51.5	2116	5	US-10-732-923-20537	Sequence 20537, A	509	32	47.1	737	3	US-09-877-884-10	Sequence 10, Appl
437	35	51.5	2118	5	US-10-732-923-20538	Sequence 20538, A	510	31	45.6	737	3	US-09-864-761-47305	Sequence 47305, A
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439	34	50.0	129	4	US-10-469-821-2	Sequence 2, Appl1	512	31	45.6	75	4	US-10-327-514-14	Sequence 14, Appl
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442	34	50.0	494	5	US-10-732-923-11146	Sequence 11146, A	515	31	45.6	79	4	US-10-425-115-232838	Sequence 232838,
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444	34	50.0	526	5	US-10-481-113-20	Sequence 20, Appl	517	31	45.6	85	4	US-10-437-963-102947	Sequence 102947,
445	34	50.0	526	5	US-10-732-923-11241	Sequence 11241, A	518	31	45.6	144	4	US-10-425-115-69116	Sequence 69116, A
446	34	50.0	526	5	US-10-481-032A-48	Sequence 48, Appl	519	31	45.6	144	4	US-10-425-115-303576	Sequence 303576,
447	34	50.0	531	5	US-10-732-923-11287	Sequence 11287, A	520	31	45.6	145	4	US-10-424-599-193305	Sequence 193305,
448	34	50.0	545	5	US-10-732-923-11256	Sequence 11256, A	521	31	45.6	165	4	US-10-795-155-707	Sequence 707, App
449	34	50.0	648	5	US-10-408-765A-2690	Sequence 2690, Ap	522	31	45.6	175	4	US-10-425-115-339534	Sequence 339534,
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451	33.5	49.3	486	6	US-11-097-143-5976	Sequence 5976, Ap	524	31	45.6	193	5	US-10-287-436A-919	Sequence 219, App
452	33	48.5	15	4	US-10-664-605-11	Sequence 11, Appl	525	31	45.6	197	4	US-10-424-599-207929	Sequence 207929,
453	33	48.5	15	4	US-10-664-605-13	Sequence 13, Appl	526	31	45.6	260	4	US-10-282-112A-66290	Sequence 66290, A
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457	33	48.5	252	4	US-10-369-493-7843	Sequence 7843, Ap	530	31	45.6	360	4	US-10-437-963-168811	Sequence 168811,
458	33	48.5	343	4	US-10-425-115-336600	Sequence 336600,	531	31	45.6	393	4	US-10-369-493-18918	Sequence 18918, A
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540	31	45.6	440	4	US-10-374-780A-1132	Sequence 1132, Ap	613	30	44.1	280	5	US-10-739-930-6124	Sequence 6124, Ap
541	31	45.6	440	4	US-10-412-699B-1331	Sequence 1331, Ap	614	30	44.1	285	4	US-10-017-161-1770	Sequence 1770, Ap
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543	31	45.6	469	3	US-09-815-242-11164	Sequence 11164, A	616	30	44.1	289	5	US-10-501-282-4030	Sequence 4030, Ap
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552	31	45.6	524	4	US-10-424-599-187261	Sequence 187261, A	625	30	44.1	391	5	US-10-732-923-11262	Sequence 11262, A
553	31	45.6	527	5	US-10-732-923-11154	Sequence 11154, A	626	30	44.1	391	5	US-10-732-923-11260	Sequence 11260, A
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563	31	45.6	582	5	US-10-481-113-22	Sequence 22, App1	636	30	44.1	417	3	US-09-333-966-4	Sequence 966-4
564	31	45.6	582	5	US-10-732-923-11246	Sequence 11246, A	637	30	44.1	417	3	US-09-993-234-6	Sequence 234-6
565	31	45.6	584	5	US-10-450-763-51710	Sequence 51710, A	638	30	44.1	417	3	US-09-314-889-4	Sequence 889-4
566	31	45.6	686	5	US-10-450-763-31213	Sequence 31213, A	639	30	44.1	417	4	US-10-005-842-5	Sequence 842-5
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572	31	45.6	1893	4	US-10-437-963-147328	Sequence 147328, A	645	30	44.1	417	4	US-10-210-951-24	Sequence 24, App1
573	31	45.6	2138	4	US-10-375-253-61	Sequence 61, App1	646	30	44.1	417	4	US-10-211-884-24	Sequence 24, App1
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575	31	45.6	2163	4	US-10-375-253-6	Sequence 6, App1	648	30	44.1	417	4	US-10-211-858-24	Sequence 24, App1
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583	30	44.1	54	4	US-10-425-115-342647	Sequence 342647, A	656	30	44.1	428	3	US-10-189-189-2	Sequence 2, App1
584	30	44.1	56	4	US-10-424-599-174562	Sequence 174562, A	657	30	44.1	428	3	US-10-189-189-2	Sequence 2, App1
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586	30	44.1	67	4	US-10-425-115-324276	Sequence 324276, A	659	30	44.1	437	4	US-10-733-923-37754	Sequence 37754, A
587	30	44.1	71	4	US-10-767-701-59852	Sequence 59852, A	660	30	44.1	443	5	US-10-733-923-27766	Sequence 27766, A
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589	30	44.1	97	5	US-10-450-763-58079	Sequence 58079, A	662	30	44.1	450	4	US-10-282-122A-50877	Sequence 50877, A
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591	30	44.1	107	4	US-10-424-599-217509	Sequence 217509, A	664	30	44.1	471	5	US-10-282-122A-62109	Sequence 62109, A
592	30	44.1	111	4	US-10-437-963-106854	Sequence 106854, A	665	30	44.1	474	4	US-10-733-923-11155	Sequence 11155, A
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594	30	44.1	130	4	US-10-424-599-268082	Sequence 268082, A	667	30	44.1	517	5	US-10-481-113-15	Sequence 15, App1
595	30	44.1	136	4	US-10-282-122A-52663	Sequence 52663, A	668	30	44.1	520	5	US-10-481-113-16	Sequence 16, App1
596	30	44.1	140	4	US-10-425-115-253192	Sequence 253192, A	669	30	44.1	521	5	US-10-733-923-11185	Sequence 11185, A
597	30	44.1	140	4	US-10-425-115-328995	Sequence 328995, A	670	30	44.1	521	5	US-10-733-923-11186	Sequence 11186, A
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694	30	44.1	541	5	US-10-310-154-537	Sequence 537, App	767	30	44.1	2031	4	US-10-140-923-101	Sequence 101, App
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711	30	44.1	584	4	US-10-093-463-84	Sequence 84, App1	784	30	44.1	2171	4	US-10-184-634-515	Sequence 515, App
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729	30	44.1	823	4	US-10-137-871-379	Sequence 379, App	802	30	44.1	2601	4	US-10-156-240-9	Sequence 9, App1
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837	29	42.6	106	5	US-10-499-762-20	Sequence 20, Appl	910	29	42.6	462	4	US-10-627-476-502	Sequence 502, App
838	29	42.6	108	4	US-10-425-115-234271	Sequence 234271,	911	29	42.6	465	5	US-10-732-923-11316	Sequence 11316, A
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877	29	42.6	316	4	US-10-425-114-57324	Sequence 57324, A	950	29	42.6	788	4	US-10-239-331B-2	Sequence 2, Appl
878	29	42.6	319	4	US-10-306-762-204	Sequence 204, App	951	29	42.6	788	4	US-10-282-122A-47546	Sequence 47546, A
879	29	42.6	324	4	US-10-437-963-122666	Sequence 122666,	952	29	42.6	792	4	US-10-437-963-182334	Sequence 182334,
880	29	42.6	336	4	US-10-425-114-61504	Sequence 61504, A	953	29	42.6	815	5	US-10-450-763-42829	Sequence 42829, A
881	29	42.6	338	4	US-10-425-114-68695	Sequence 68695, A	954	29	42.6	816	4	US-10-282-122A-52967	Sequence 52967, A
882	29	42.6	343	4	US-10-156-761-7772	Sequence 7772, A	955	29	42.6	828	4	US-10-437-963-152744	Sequence 152744,
883	29	42.6	361	4	US-10-094-749-3049	Sequence 3049, Ap	956	29	42.6	869	4	US-10-437-963-189803	Sequence 189803,
884	29	42.6	361	4	US-10-038-854-165	Sequence 165, App	957	29	42.6	972	4	US-10-369-493-11947	Sequence 11947, A
885	29	42.6	367	5	US-10-450-763-44988	Sequence 44988, A	958	29	42.6	980	4	US-10-282-122A-50522	Sequence 50522, A
886	29	42.6	373	4	US-10-282-122A-47451	Sequence 47451, A	959	29	42.6	999	4	US-10-122-155-395	Sequence 395, App
887	29	42.6	378	4	US-10-369-493-5080	Sequence 5080, Ap	960	29	42.6	999	4	US-10-146-731-395	Sequence 395, App
888	29	42.6	386	5	US-10-732-923-11268	Sequence 11268, A	961	29	42.6	999	4	US-10-140-472-395	Sequence 395, App
889	29	42.6	393	5	US-10-732-923-7212	Sequence 7212, Ap	962	29	42.6	999	4	US-10-141-761-395	Sequence 395, App
890	29	42.6	397	5	US-10-450-763-60388	Sequence 60388, A	963	29	42.6	999	4	US-10-147-953-395	Sequence 395, App
891	29	42.6	399	5	US-10-450-763-49842	Sequence 49842, A	964	29	42.6	999	4	US-10-142-885-395	Sequence 395, App
892	29	42.6	400	5	US-10-282-122A-77595	Sequence 55885, A	965	29	42.6	999	4	US-10-137-871-395	Sequence 395, App
893	29	42.6	414	4	US-10-282-122A-77595	Sequence 77595, A	966	29	42.6	999	4	US-10-140-923-395	Sequence 395, App
894	29	42.6	419	3	US-09-741-669-415	Sequence 415, App	967	29	42.6	999	4	US-10-140-923-395	Sequence 395, App
895	29	42.6	419	4	US-10-369-493-23477	Sequence 23477, A	968	29	42.6	999	4	US-10-141-759-395	Sequence 395, App
896	29	42.6	419	4	US-10-038-854-371	Sequence 371, App	969	29	42.6	999	4	US-10-140-805-395	Sequence 395, App
897	29	42.6	429	5	US-09-738-626-5318	Sequence 5318, Ap	970	29	42.6	999	4	US-10-140-864-395	Sequence 395, App
898	29	42.6	431	3	US-10-494-541-50	Sequence 50, Appl	971	29	42.6	1015	6	US-11-097-143-24927	Sequence 24927, A
899	29	42.6	431	3	US-09-815-242-5145	Sequence 5145, Ap	972	29	42.6	1193	4	US-10-437-963-159706	Sequence 159706,
900	29	42.6	431	4	US-10-282-122A-33538	Sequence 43538, A	973	29	42.6	1355	4	US-10-123-155-421	Sequence 421, App
901	29	42.6	431	4	US-10-425-114-51428	Sequence 51428, A	974	29	42.6	1355	4	US-10-146-721-421	Sequence 421, App
902	29	42.6	434	4	US-10-282-122A-60268	Sequence 60268, A	975	29	42.6	1355	4	US-10-140-472-421	Sequence 421, App
903	29	42.6	435	5	US-10-810-352-60	Sequence 60, Appl	976	29	42.6	1355	4	US-10-141-761-421	Sequence 421, App

977 29 42.6 1355 4 US-10-142-885-421 Sequence 421, App
978 29 42.6 1355 4 US-10-158-790-421 Sequence 421, App
979 29 42.6 1355 4 US-10-137-871-421 Sequence 421, App
980 29 42.6 1355 4 US-10-140-923-421 Sequence 421, App
981 29 42.6 1355 4 US-10-141-756-421 Sequence 421, App
982 29 42.6 1355 4 US-10-141-756-421 Sequence 421, App
983 29 42.6 1355 4 US-10-140-805-421 Sequence 421, App
984 29 42.6 1355 4 US-10-140-864-421 Sequence 421, App
985 29 42.6 1356 4 US-10-123-155-43 Sequence 43, App1
986 29 42.6 1356 4 US-10-146-731-43 Sequence 43, App1
987 29 42.6 1356 4 US-10-140-472-43 Sequence 43, App1
988 29 42.6 1356 4 US-10-141-761-43 Sequence 43, App1
989 29 42.6 1356 4 US-10-142-885-43 Sequence 43, App1
990 29 42.6 1356 4 US-10-158-790-43 Sequence 43, App1
991 29 42.6 1356 4 US-10-137-871-43 Sequence 43, App1
992 29 42.6 1356 4 US-10-140-923-43 Sequence 43, App1
993 29 42.6 1356 4 US-10-141-756-43 Sequence 43, App1
994 29 42.6 1356 4 US-10-141-759-43 Sequence 43, App1
995 29 42.6 1356 4 US-10-140-805-43 Sequence 43, App1
996 29 42.6 1356 4 US-10-140-864-43 Sequence 43, App1
997 29 42.6 1356 4 US-10-437-963-107743 Sequence 107743,
998 29 42.6 1410 4 US-10-184-644-123 Sequence 123, App
999 29 42.6 1410 4 US-10-184-634-123 Sequence 123, App
1000 29 42.6 1422 4 US-10-123-155-117 Sequence 117, App

ALIGNMENTS

RESULT 1
US-10-664-605-10
; Sequence 10, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golemo, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-10
Query Match 82.4%; Score 56; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.0003;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
DB 1 CFGLKADRIGSASGLGC 17

RESULT 2
US-10-664-605-40
; Sequence 40, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golemo, Myriam

; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-40
Query Match 82.4%; Score 56; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.0003;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
DB 1 CFGLKADRIGSASGLGC 17

RESULT 3
US-10-664-605-45
; Sequence 45, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golemo, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-45
Query Match 82.4%; Score 56; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.0003;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXGC 17
DB 1 CFGLKADRIGSASGLGC 17

RESULT 4
US-10-664-605-58
; Sequence 58, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.

```

; APPLICANT: Golemb, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-58
```

```

Query Match      82.4%; Score 56; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.0003;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
Qy      1 CFGXXXDRIGXXSXXGC 17
      ||| ||| ||| |||
Db      1 CFGKLDRIGSSSALGC 17
```

RESULT 5
US-10-664-605-63

```

; Sequence 63, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golemb, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-63
```

```

Query Match      82.4%; Score 56; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.0003;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
Qy      1 CFGXXXDRIGXXSXXGC 17
      ||| ||| ||| |||
Db      1 CFGKLDRIGSSGAGC 17
```

RESULT 6
US-10-664-605-68

```

; Sequence 68, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golemb, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-68
```

```

Query Match      82.4%; Score 56; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.0003;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
Qy      1 CFGXXXDRIGXXSXXGC 17
      ||| ||| ||| |||
Db      1 CFGKLDRIGSSSGLGC 17
```

RESULT 7
US-11-066-697-469

```

; Sequence 469, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 469
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-066-697-469
```

```

Query Match      82.4%; Score 56; DB 6; Length 20;
Best Local Similarity 58.8%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
Qy      1 CFGXXXDRIGXXSXXGC 17
      ||| ||| ||| |||
Db      1 CFGSRIDRIGAGSGWGC 17
```

```
RESULT 8
US-11-066-697-470
; Sequence 470, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 470
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-470
```

```
Query Match      82.4%; Score 56; DB 6; Length 21;
Best Local Similarity 58.8%; Pred. No. 0.00037;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
Qy      1 CFGXXXXRIGXXSXXGC 17
      ||| ||| ||| |||
Db      1 CFGSRIDRIGAQSGMGC 17
```

```
RESULT 9
US-09-752-724-5
; Sequence 5, Application US/09752724
; Patent No. US20010027181A1
; GENERAL INFORMATION:
; APPLICANT: KITAKAZE, Masafumi
; APPLICANT: Bridon, Dominique P.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR USE IN TREATMENT OR PROPHYLAXIS
; TITLE OF INVENTION: ISCHEMIC HEART DISEASE
; FILE REFERENCE: PP-S-38-25205
; CURRENT APPLICATION NUMBER: US/09/752,724
; CURRENT FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: JP 98134/2000
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 24
; TYPE: PRT
; ORGANISM: frog
US-09-752-724-5
```

```
Query Match      82.4%; Score 56; DB 3; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00042;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
Qy      1 CFGXXXXRIGXXSXXGC 17
      ||| ||| ||| |||
Db      4 CFGSRIDRIGAQSGMGC 20
```

```
RESULT 10
US-11-066-697-468
; Sequence 468, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 468
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-468
```

```
Query Match      82.4%; Score 56; DB 6; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00042;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
Qy      1 CFGXXXXRIGXXSXXGC 17
      ||| ||| ||| |||
Db      4 CFGSRIDRIGAQSGMGC 20
```

```
RESULT 11
US-11-066-697-471
; Sequence 471, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Milner, Peter G.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 471
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
```

```
Qy      1 CFGXXXXRIGXXSXXGC 17
      ||| ||| ||| |||
Db      4 CFGSRIDRIGAQSGMGC 20
```


US-11-066-697-471

Query Match 82.4%; Score 56; DB 6; Length 24;

Best Local Similarity 58.8%; Pred. No. 0.00042;

Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 CPGXXXDRIGXXSXXGC 17
||| ||| ||| |||
Db 4 CPGSRIDRIGASGMGC 20

RESULT 12

US-11-066-697-472

Sequence 472, Application US/11066697

Publication No. US20050187159A1

GENERAL INFORMATION:

APPLICANT: Bridon, Dominique P.

APPLICANT: Ezrin, Alan M.

APPLICANT: Milner, Peter G.

APPLICANT: Holmes, Darren L.

APPLICANT: Thibaudau, Karen

TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM

TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD

TITLE OF INVENTION: COMPONENTS

FILE REFERENCE: 500862002301

CURRENT APPLICATION NUMBER: US/11/066,697

CURRENT FILING DATE: 2005-02-25

PRIOR APPLICATION NUMBER: 09/657,276

PRIOR FILING DATE: 2000-09-07

PRIOR APPLICATION NUMBER: 60/153,406

PRIOR FILING DATE: 1999-09-10

PRIOR APPLICATION NUMBER: 60/159,783

PRIOR FILING DATE: 1999-10-15

NUMBER OF SEQ ID NOS: 1617

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 472

LENGTH: 30

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Peptide

US-11-066-697-472

Query Match 82.4%; Score 56; DB 6; Length 30;

Best Local Similarity 58.8%; Pred. No. 0.00052;

Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 CPGXXXDRIGXXSXXGC 17
||| ||| ||| |||
Db 11 CPGSRIDRIGASGMGC 27

RESULT 13

US-09-902-517-15

Sequence 15, Application US/09902517

Publication No. US20030109430A1

GENERAL INFORMATION:

APPLICANT: Seilhamer, Jeffrey J.

APPLICANT: Lewicki, John

APPLICANT: Scarborough, Robert M.

APPLICANT: Porter, Gordon J.

TITLE OF INVENTION: IMMUNOSSAYS FOR HUMAN AND CANINE BRAIN

TITLE OF INVENTION: NATRIURETIC PEPTIDE

FILE REFERENCE: 219002025213

CURRENT APPLICATION NUMBER: US/09/902,517

CURRENT FILING DATE: 2001-07-09

PRIOR APPLICATION NUMBER: 09/287,892

PRIOR FILING DATE: 1999-04-07

PRIOR APPLICATION NUMBER: 08/850,910

PRIOR FILING DATE: 1997-05-05

PRIOR APPLICATION NUMBER: 07/477,226

PRIOR FILING DATE: 1990-02-08

PRIOR APPLICATION NUMBER: 07/299,880

PRIOR FILING DATE: 1989-01-19

PRIOR APPLICATION NUMBER: 07/206,470

PRIOR FILING DATE: 1988-06-14

PRIOR APPLICATION NUMBER: 07/200,383

PRIOR FILING DATE: 1988-05-31

NUMBER OF SEQ ID NOS: 50

SOFTWARE: FastSeq for Windows, Version 4.0

SEQ ID NO 15

LENGTH: 17

TYPE: PRT

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Proviso formula (1)

US-09-902-517-15

Query Match 80.9%; Score 55; DB 3; Length 17;

Best Local Similarity 58.8%; Pred. No. 0.00047;

Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 CPGXXXDRIGXXSXXGC 17
||| ||| ||| |||
Db 1 CPGSRIDRIGSLSGGC 17

RESULT 14

US-09-027-777B-1

Sequence 1, Application US/0902777B

Publication No. US20030171536A1

GENERAL INFORMATION:

APPLICANT: IMMER, Hansueli

APPLICANT: FORSMANN, Wolf-Georg

APPLICANT: ADERMAN, Knut

APPLICANT: KLESSEN, Christian

TITLE OF INVENTION: PROCESS AND INTERMEDIATE PRODUCTS FOR

TITLE OF INVENTION: PREPARING CARDIOLATIN FRAGMENTS AND HIGHLY PURIFIED CARDIO

TITLE OF INVENTION: FRAGMENTS

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Nikaido, Marmelstein, Murray & Oram

STREET: 655 Fifteenth Street, N.W., Suite 330

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-4810

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/027,777B

FILING DATE: 23-FEB-1998

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 44 20 381.0

FILING DATE: 02-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 195 13 784.1

FILING DATE: 10-APR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Kites, Monica C.

REGISTRATION NUMBER: 36,105

REFERENCE/DOCKET NUMBER: P1614-8019

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 638-5000

TELEFAX: (202) 368-4810

INFORMATION FOR SEQ ID NO. 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide
US-09-027-777B-1

Query Match 80.9%; Score 55; DB 3; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXSXXGC 17
DB 1 CFGGRMDRIGASGLGC 17

RESULT 15
US-10-327-514-17

; Sequence 17, Application US/10327514
; Publication No. US20030125258A1
; GENERAL INFORMATION:
; APPLICANT: LANCOT, Christian
; APPLICANT: SALOIS, Patrick
; APPLICANT: MOFRATT, Pierre
; TITLE OF INVENTION: BONE POLYPEPTIDE-1
; FILE REFERENCE: 544172000100
; CURRENT APPLICATION NUMBER: US/10/327,514
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/341,224
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-327-514-17

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXSXXGC 17
DB 1 CFGGRMDRIGASGLGC 17

RESULT 16
US-10-327-514-18

; Sequence 18, Application US/10327514
; Publication No. US20030125258A1
; GENERAL INFORMATION:
; APPLICANT: LANCOT, Christian
; APPLICANT: SALOIS, Patrick
; APPLICANT: MOFRATT, Pierre
; TITLE OF INVENTION: BONE POLYPEPTIDE-1
; FILE REFERENCE: 544172000100
; CURRENT APPLICATION NUMBER: US/10/327,514
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/341,224
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-327-514-18

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXSXXGC 17
DB 1 CFGGRMDRIGASGLGC 17

RESULT 17
US-10-327-514-19

; Sequence 19, Application US/10327514
; Publication No. US20030125258A1
; GENERAL INFORMATION:
; APPLICANT: LANCOT, Christian
; APPLICANT: SALOIS, Patrick
; APPLICANT: MOFRATT, Pierre
; TITLE OF INVENTION: BONE POLYPEPTIDE-1
; FILE REFERENCE: 544172000100
; CURRENT APPLICATION NUMBER: US/10/327,514
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/341,224
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-327-514-19

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXSXXGC 17
DB 1 CFGGLDRIGSMGLGC 17

RESULT 18
US-10-402-021-15

; Sequence 15, Application US/10402021
; Publication No. US20040002458A1
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Lewicki, John
; APPLICANT: Scarborough, Robert M.
; APPLICANT: Porter, Gordon J.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS USING NATRIURETIC PEPTIDE
; FILE REFERENCE: 219002025203
; CURRENT APPLICATION NUMBER: US/10/402,021
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: 09/287,892
; PRIOR FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: 08/850,910
; PRIOR FILING DATE: 1997-05-05
; PRIOR APPLICATION NUMBER: 07/477,226
; PRIOR FILING DATE: 1990-02-08
; PRIOR APPLICATION NUMBER: 07/299,880
; PRIOR FILING DATE: 1989-01-19
; PRIOR APPLICATION NUMBER: 07/206,470
; PRIOR FILING DATE: 1988-06-14
; PRIOR APPLICATION NUMBER: 07/200,383
; PRIOR FILING DATE: 1988-05-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Proviso formula (1)
US-10-402-021-15

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXSXXGC 17

Db 1 CFGRRLDRIKSLGSLG 17

RESULT 19

US-10-664-605-2
; Sequence 2, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: P23582
; DATABASE ENTRY DATE: 2001-10-16
; RELEVANT RESIDUES: (110)..(126)
US-10-664-605-2

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXXRIGXSXXGC 17
Db 1 CFGKLDRIKSLGSLG 17

RESULT 20

US-10-664-605-41
; Sequence 41, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-41

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;

Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXXRIGXSXXGC 17
Db 1 CFGKLDRIKSLGSLG 17

RESULT 21

US-10-664-605-42
; Sequence 42, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-42

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXXRIGXSXXGC 17
Db 1 CFGKLDRIKSLGSLG 17

RESULT 22

US-10-664-605-43
; Sequence 43, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-43

Query Match 80.9%; Score 55; DB 4; Length 17;

OTHER INFORMATION: peptide variant
US-10-6664-605-54

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXXGC 17
Db 1 CFGKLDRIGMSGLGC 17

RESULT 27

US-10-664-605-56
; Sequence 56, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-56

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXXGC 17
Db 1 CFGKLDRIGTMSGLGC 17

RESULT 28

US-10-664-605-59
; Sequence 59, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant

US-10-664-605-59

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXXGC 17
Db 1 CFGKLDRIGMSGLGC 17

RESULT 29

US-10-664-605-60
; Sequence 60, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-60

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXXGC 17
Db 1 CFGKLDRIGMSKLGK 17

RESULT 30

US-10-664-605-61
; Sequence 61, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembo, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: peptide variant
US-10-664-605-61

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXXGC 17
Db 1 CFGKLDRIGSMGCGC 17

RESULT 31
US-10-664-605-62

; Sequence 62, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembio, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-62

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXXGC 17
Db 1 CFGKLDRIGSMGCGC 17

RESULT 32
US-10-664-605-64

; Sequence 64, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembio, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-64

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXXGC 17
Db 1 CFGKLDRIGSMGCGC 17

RESULT 33
US-10-664-605-66

; Sequence 66, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembio, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide variant
US-10-664-605-66

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXXGC 17
Db 1 CFGKLDRIGSHGCGC 17

RESULT 34
US-10-664-605-67

; Sequence 67, Application US/10664605
; Publication No. US20040138134A1
; GENERAL INFORMATION:
; APPLICANT: Prochon Biotech Ltd.
; APPLICANT: Golembio, Myriam
; APPLICANT: Yavon, Avner
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
; FILE REFERENCE: PRO/011/US
; CURRENT APPLICATION NUMBER: US/10/664,605
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/276,939
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: IL 142118
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/IL02/00229
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 17
; TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: peptide variant
US-10-664-605-67

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXXRIGXSXXGC 17
Db 1 CFGKLDRIGSKSGLGC 17

RESULT 35
US-10-664-605-69

Sequence 69, Application US/10664605
Publication No. US20040138134A1
GENERAL INFORMATION:
APPLICANT: Prochon Biotech Ltd.
APPLICANT: Golemb, Myriam
APPLICANT: Yaron, Avner
TITLE OF INVENTION: METHOD AND COMPOSITION FOR TREATMENT OF SKELETAL DYSPLASIAS
FILE REFERENCE: PRO/011/US
CURRENT APPLICATION NUMBER: US/10/664,605
CURRENT FILING DATE: 2003-09-15
PRIOR APPLICATION NUMBER: US 60/276,939
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: IL 142118
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: PCT/IL02/00229
PRIOR FILING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.1
SEQ ID NO 69
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: peptide variant
US-10-664-605-69

Query Match 80.9%; Score 55; DB 4; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXXRIGXSXXGC 17
Db 1 CFGKLDRIGSKSGLGC 17

RESULT 36
US-10-499-762-17

Sequence 17, Application US/10499762
Publication No. US20050143562A1
GENERAL INFORMATION:
APPLICANT: PHENOGENE THERAPEUTICS INC.
APPLICANT: LANCTOT, Christian
APPLICANT: SALOIS, Patrick
APPLICANT: MOFFATT, Pierre
TITLE OF INVENTION: BONE POLYPEPTIDE-1
FILE REFERENCE: 09680.0252USMO
CURRENT APPLICATION NUMBER: US/10/499,762
CURRENT FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: PCT/IB02/05778
PRIOR FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 60/341,224
PRIOR FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 17
TYPE: PRT

ORGANISM: Rattus norvegicus
US-10-499-762-17

Query Match 80.9%; Score 55; DB 5; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXXRIGXSXXGC 17
Db 1 CFGGRIDRIGAGSLGC 17

RESULT 37
US-10-499-762-18

Sequence 18, Application US/10499762
Publication No. US20050143562A1
GENERAL INFORMATION:
APPLICANT: PHENOGENE THERAPEUTICS INC.
APPLICANT: LANCTOT, Christian
APPLICANT: SALOIS, Patrick
APPLICANT: MOFFATT, Pierre
TITLE OF INVENTION: BONE POLYPEPTIDE-1
FILE REFERENCE: 09680.0252USMO
CURRENT APPLICATION NUMBER: US/10/499,762
CURRENT FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: PCT/IB02/05778
PRIOR FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 60/341,224
PRIOR FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 17
TYPE: PRT
ORGANISM: Rattus norvegicus
US-10-499-762-18

Query Match 80.9%; Score 55; DB 5; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXXRIGXSXXGC 17
Db 1 CFGKIDRIGAVSRIGC 17

RESULT 38
US-10-499-762-19

Sequence 19, Application US/10499762
Publication No. US20050143562A1
GENERAL INFORMATION:
APPLICANT: PHENOGENE THERAPEUTICS INC.
APPLICANT: LANCTOT, Christian
APPLICANT: SALOIS, Patrick
APPLICANT: MOFFATT, Pierre
TITLE OF INVENTION: BONE POLYPEPTIDE-1
FILE REFERENCE: 09680.0252USMO
CURRENT APPLICATION NUMBER: US/10/499,762
CURRENT FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: PCT/IB02/05778
PRIOR FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 60/341,224
PRIOR FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 17
TYPE: PRT
ORGANISM: Rattus norvegicus
US-10-499-762-19

Query Match 80.9%; Score 55; DB 5; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00047;

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      PRIOR APPLICATION NUMBER: 07/200,183
      PRIOR FILING DATE: 1988-05-31
      NUMBER OF SEQ. ID NOS: 50
      SOFTWARE: FastSeq for Windows Version 4.0
      SEQ ID NO 32
      LENGTH: 20
      TYPE: PRT
      ORGANISM: Unknown
      FEATURE:
      OTHER INFORMATION: Amino acids encoding pBNP
      US-09-902-517-32

Query Match      80.9%; Score 55; DB 3; Length 20;
Best Local Similarity 58.8%; Pred. No. 0.00056;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFCGXXDRIGXXSXGC 17
      ||| ||| ||| |||
Db      3 CFCGRMDRIGXQSGLC 19

RESULT 41
US-09-902-517-34
; Sequence 34, Application US/09902517
; Publication No. US20030109430A1
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Lewicki, John
; APPLICANT: Scarborough, Robert M.
; APPLICANT: Porter, Gordon J.
; TITLE OF INVENTION: IMMUNOAAYS FOR HUMAN AND CANINE BRAIN
; TITLE OF INVENTION: NATRIURETIC PEPTIDE
; FILE REFERENCE: 219002025213
; CURRENT APPLICATION NUMBER: US/09/902,517
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 09/287,892
; PRIOR FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: 08/850,910
; PRIOR FILING DATE: 1997-05-05
; PRIOR APPLICATION NUMBER: 07/477,226
; PRIOR FILING DATE: 1990-02-08
; PRIOR APPLICATION NUMBER: 07/299,880
; PRIOR FILING DATE: 1989-01-19
; PRIOR APPLICATION NUMBER: 07/206,470
; PRIOR FILING DATE: 1988-06-14
; PRIOR APPLICATION NUMBER: 07/200,383
; PRIOR FILING DATE: 1988-05-31
; NUMBER OF SEQ. ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Amino acids encoding pBNP
      US-09-902-517-34

Query Match      80.9%; Score 55; DB 3; Length 20;
Best Local Similarity 58.8%; Pred. No. 0.00056;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFCGXXDRIGXXSXGC 17
      ||| ||| ||| |||
Db      3 CFCGRMDRIGXQSGLC 19

RESULT 42
US-10-402-021-32
; Sequence 32, Application US/10402021
; Publication No. US20040002458A1
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Lewicki, John

```


APPLICANT: Scarborough, Robert M.
APPLICANT: Porter, Gordon J.
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS USING NATRIURETIC PEPTIDE
TITLE OF INVENTION: (AMENDED)
FILE REFERENCE: 219002025203
CURRENT APPLICATION NUMBER: US/10/402,021
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: 09/287,892
PRIOR FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: 08/850,910
PRIOR FILING DATE: 1997-05-05
PRIOR APPLICATION NUMBER: 07/477,226
PRIOR FILING DATE: 1990-02-08
PRIOR APPLICATION NUMBER: 07/299,880
PRIOR FILING DATE: 1988-01-19
PRIOR APPLICATION NUMBER: 07/206,470
PRIOR FILING DATE: 1988-06-14
PRIOR APPLICATION NUMBER: 07/200,383
PRIOR FILING DATE: 1988-05-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 32
LENGTH: 20
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Amino acids encoding pBNP
US-10-402-021-32

Query Match 80.9%; Score 55; DB 4; Length 20;
Best Local Similarity 58.8%; Pred. No. 0.00056;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXXGC 17
||| ||| | ||
Db 3 CFGGRMDRIGAGSGIGC 19

RESULT 43
US-10-402-021-34
Sequence 34, Application US/10402021
Publication No. US20040002458A1
GENERAL INFORMATION:
APPLICANT: Selbamer, Jeffrey J.
APPLICANT: Lewicki, John
APPLICANT: Scarborough, Robert M.
APPLICANT: Porter, Gordon J.
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS USING NATRIURETIC PEPTIDE
TITLE OF INVENTION: (AMENDED)
FILE REFERENCE: 219002025203
CURRENT APPLICATION NUMBER: US/10/402,021
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: 09/287,892
PRIOR FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: 08/850,910
PRIOR FILING DATE: 1997-05-05
PRIOR APPLICATION NUMBER: 07/477,226
PRIOR FILING DATE: 1990-02-08
PRIOR APPLICATION NUMBER: 07/299,880
PRIOR FILING DATE: 1988-01-19
PRIOR APPLICATION NUMBER: 07/206,470
PRIOR FILING DATE: 1988-06-14
PRIOR APPLICATION NUMBER: 07/200,383
PRIOR FILING DATE: 1988-05-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 20
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Amino acids encoding pBNP
US-10-402-021-34

Query Match 80.9%; Score 55; DB 4; Length 20;
Best Local Similarity 58.8%; Pred. No. 0.00056;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXXGC 17
||| ||| | ||
Db 3 CFGRLDRIGAGSGIGC 19

RESULT 44
US-11-066-697-483
Sequence 483, Application US/11066697
Publication No. US20050187159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezrin, Alan M.
APPLICANT: Milner, Peter G.
APPLICANT: Holmes, Darren L.
APPLICANT: Thibodeau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
FILE REFERENCE: 500862002301
CURRENT APPLICATION NUMBER: US/11/066,697
CURRENT FILING DATE: 2005-02-25
PRIOR APPLICATION NUMBER: 09/657,276
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 483
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-483

Query Match 80.9%; Score 55; DB 6; Length 21;
Best Local Similarity 58.8%; Pred. No. 0.00058;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXXGC 17
||| ||| | ||
Db 3 CFGRLDRIGAGSGIGC 19

RESULT 45
US-09-752-724-3
Sequence 3, Application US/09752724
Patent No. US20010027181A1
GENERAL INFORMATION:
APPLICANT: KITAKAZE, Masafumi
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR USE IN TREATMENT OR PROPHYLAXIS
TITLE OF INVENTION: ISCHEMIC HEART DISEASE
FILE REFERENCE: PP/S-38-252US
CURRENT APPLICATION NUMBER: US/09/752,724
CURRENT FILING DATE: 2001-01-03
PRIOR APPLICATION NUMBER: JP 98134/2000
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 22
TYPE: PRT
ORGANISM: frog
FEATURE:
OTHER INFORMATION: Amino acids encoding pBNP
US-09-752-724-3

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Query Match      80.9%; Score 55; DB 3; Length 22;
Best Local Similarity 58.8%; Pred. No. 0.00061;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      1 CFGXXXDRIGXXSXXGC 17
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Db      1 CFGGMDRIGAGSGGCG 17

RESULT 46
US-09-752-724-9
; Sequence 9, Application US/09752724
; Patent No. US20010027181A1
; GENERAL INFORMATION:
; APPLICANT: KITAKAZE, Masafumi
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR USE IN TREATMENT OR PROPHYLAXIS
; FILE REFERENCE: PP/S-38-252US
; CURRENT APPLICATION NUMBER: US/09/752,724
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: JP 98134/2000
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens, porcine, rat
US-09-752-724-9

Query Match      80.9%; Score 55; DB 3; Length 22;
Best Local Similarity 58.8%; Pred. No. 0.00061;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      1 CFGXXXDRIGXXSXXGC 17
      ||| ||| ||| ||| |||
Db      6 CFGKLDRIGMSGGCG 22

RESULT 47
US-09-752-724-10
; Sequence 10, Application US/09752724
; Patent No. US20010027181A1
; GENERAL INFORMATION:
; APPLICANT: KITAKAZE, Masafumi
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR USE IN TREATMENT OR PROPHYLAXIS
; FILE REFERENCE: PP/S-38-252US
; CURRENT APPLICATION NUMBER: US/09/752,724
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: JP 98134/2000
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: PRT
; ORGANISM: chicken
US-09-752-724-10

Query Match      80.9%; Score 55; DB 3; Length 22;
Best Local Similarity 58.8%; Pred. No. 0.00061;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      1 CFGXXXDRIGXXSXXGC 17
      ||| ||| ||| ||| |||
Db      6 CFGVLDRIIGMSGGCG 22

RESULT 48
US-09-752-724-11
; Sequence 11, Application US/09752724
; Patent No. US20010027181A1

; GENERAL INFORMATION:
; APPLICANT: KITAKAZE, Masafumi
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR USE IN TREATMENT OR PROPHYLAXIS
; FILE REFERENCE: PP/S-38-252US
; CURRENT APPLICATION NUMBER: US/09/752,724
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: JP 98134/2000
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 22
; TYPE: PRT
; ORGANISM: frog
US-09-752-724-11

Query Match      80.9%; Score 55; DB 3; Length 22;
Best Local Similarity 58.8%; Pred. No. 0.00061;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      1 CFGXXXDRIGXXSXXGC 17
      ||| ||| ||| ||| |||
Db      6 CFGVLDRIIGMSGGCG 22

RESULT 49
US-09-466-268B-9
; Sequence 9, Application US/09466268B
; Publication No. US20020082219A1
; GENERAL INFORMATION:
; APPLICANT: Burnett, Jr., John C.
; APPLICANT: Lisy, Ondrej
; TITLE OF INVENTION: Chimeric natriuretic peptides
; FILE REFERENCE: 150.199US1
; CURRENT APPLICATION NUMBER: US/09/466,268B
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-466-268B-9

Query Match      80.9%; Score 55; DB 3; Length 22;
Best Local Similarity 58.8%; Pred. No. 0.00061;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      1 CFGXXXDRIGXXSXXGC 17
      ||| ||| ||| ||| |||
Db      6 CFGKLDRIGMSGGCG 22

RESULT 50
US-09-912-425-3
; Sequence 3, Application US/09912425
; Patent No. US20020128176A1
; GENERAL INFORMATION:
; APPLICANT: Forssmann, Wolf-Georg
; APPLICANT: Maegerl, Hans-Juergen
; APPLICANT: Stief, Christian
; APPLICANT: Kueche, Andrea
; APPLICANT: Ueckert, Stefan
; APPLICANT: Becker, Armin
; APPLICANT: Jonas, Udo
; TITLE OF INVENTION: Treatment of Erectile Dysfunction with C-Type
; TITLE OF INVENTION: Natriuretic Polypeptide (CNP) as a Monotherapy or in
; FILE REFERENCE: 011634us
; CURRENT APPLICATION NUMBER: US/09/912,425
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: DE19903087.1
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Fri Jan 27 10:40:56 2006

; PRIOR FILING DATE: 1999-01-27
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: Patentln Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 22
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-912-425-3

Query Match 80.9%; Score 55; DB 3; Length 22;
 Best Local Similarity 58.8%; Pred. No. 0.00061;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 Qy 1 CFGXXXDRIGXXXGXC 17
 Db 6 CFGKLDRIGSMGGLGC 22

Search completed: January 26, 2006, 14:47:16
 Job time : 67 secs

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OM protein - protein search, using sw model

Run on: January 26, 2006, 14:43:48 : Search time 7 Seconds
(without alignments)
26.299 Million cell updates/sec

Title: US-10-664-605-5

Perfect score: 68

Sequence: 1 CFGXXRXDRIGXXSXXGC 17

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New:*

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6: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	80.9	28	7	US-11-112-227-16
2	55	80.9	28	7	US-11-112-227-50
3	55	80.9	28	7	US-11-112-227-51
4	55	80.9	28	7	US-11-059-814-4
5	55	80.9	28	7	US-11-175-690-309
6	55	80.9	121	6	US-10-510-880-3
7	55	80.9	126	6	US-10-977-334-5
8	55	80.9	131	6	US-10-510-880-2
9	55	80.9	151	7	US-11-059-814-7
10	55	80.9	152	7	US-11-059-814-16
11	55	80.9	153	6	US-10-977-334-4
12	55	80.9	637	7	US-11-175-690-222
13	55	79.5	26	7	US-11-175-690-321
14	50	73.5	27	7	US-11-175-690-332
15	50	73.5	27	7	US-11-175-690-371
16	50	73.5	28	7	US-11-175-690-333
17	50	73.5	28	7	US-11-175-690-369
18	50	73.5	29	7	US-11-175-690-314
19	50	73.5	29	7	US-11-175-690-315
20	50	73.5	32	6	US-10-510-880-4
21	50	73.5	32	6	US-10-977-334-3
22	50	73.5	32	7	US-11-043-590-17
23	50	73.5	32	7	US-11-175-690-288
24	50	73.5	32	7	US-11-175-690-298
25	50	73.5	32	7	US-11-175-690-304

26	50	73.5	32	7	US-11-175-690-317	Sequence 317, App
27	50	73.5	32	7	US-11-175-690-318	Sequence 318, App
28	50	73.5	32	7	US-11-175-690-370	Sequence 370, App
29	50	73.5	42	7	US-11-043-590-15	Sequence 15, Appl
30	50	73.5	52	7	US-11-175-690-368	Sequence 368, App
31	50	73.5	60	7	US-11-043-590-16	Sequence 16, Appl
32	50	73.5	108	6	US-10-510-880-5	Sequence 5, Appl1
33	50	73.5	108	6	US-10-875-800-1	Sequence 1, Appl1
34	50	73.5	108	6	US-10-299-977-1	Sequence 1, Appl1
35	50	73.5	134	6	US-10-510-880-1	Sequence 2, Appl1
36	50	73.5	134	6	US-10-875-800-2	Sequence 1, Appl1
37	50	73.5	134	6	US-11-043-590-12	Sequence 12, Appl1
38	50	73.5	162	7	US-11-043-590-13	Sequence 13, Appl1
39	50	73.5	630	7	US-11-175-690-234	Sequence 234, App
40	50	73.5	630	7	US-11-175-690-235	Sequence 235, App
41	50	73.5	632	7	US-11-175-690-236	Sequence 236, App
42	50	73.5	633	7	US-11-175-690-228	Sequence 228, App
43	50	73.5	641	7	US-11-175-690-211	Sequence 211, App
44	50	73.5	641	7	US-11-175-690-230	Sequence 230, App
45	50	73.5	661	7	US-11-175-690-281	Sequence 281, App
46	50	73.5	663	7	US-11-175-690-284	Sequence 284, App
47	50	73.5	665	7	US-11-175-690-282	Sequence 282, App
48	50	73.5	667	7	US-11-175-690-227	Sequence 227, App
49	50	73.5	670	7	US-11-175-690-283	Sequence 283, App
50	50	73.5	673	7	US-11-175-690-201	Sequence 201, App
51	50	73.5	673	7	US-11-175-690-217	Sequence 217, App
52	50	73.5	673	7	US-11-175-690-231	Sequence 231, App
53	32	47.1	91	6	US-10-485-788A-818	Sequence 818, App
54	32	47.1	91	6	US-11-053-076-203	Sequence 203, App
55	31	45.6	770	7	US-11-024-959-358	Sequence 358, App
56	31	45.6	2221	7	US-11-126-313-57	Sequence 30, Appl1
57	30	44.1	32	6	US-10-512-325-5	Sequence 5, Appl1
58	30	44.1	32	7	US-11-196-918-4	Sequence 4, Appl1
59	30	44.1	418	6	US-10-512-325-3	Sequence 3, Appl1
60	30	44.1	418	7	US-11-196-919-2	Sequence 2, Appl1
61	30	44.1	487	6	US-10-055-877-268	Sequence 268, App
62	30	44.1	556	6	US-10-055-877-81	Sequence 81, Appl
63	30	44.1	573	6	US-10-055-877-79	Sequence 79, Appl
64	30	44.1	833	7	US-11-076-187-5	Sequence 5, Appl1
65	30	44.1	1176	6	US-10-821-234-897	Sequence 897, Appl
66	29	42.6	85	6	US-10-467-657-3010	Sequence 269, App
67	29	42.6	347	6	US-10-055-877-269	Sequence 270, App
68	29	42.6	347	6	US-10-055-877-270	Sequence 271, App
69	29	42.6	347	6	US-10-055-877-271	Sequence 274, App
70	29	42.6	550	6	US-10-055-877-214	Sequence 275, App
71	29	42.6	551	6	US-10-055-877-276	Sequence 276, App
72	29	42.6	551	6	US-10-055-877-273	Sequence 273, App
73	29	42.6	563	6	US-11-070-080-19	Sequence 19, Appl
74	28	41.2	273	7	US-11-108-528-44	Sequence 44, Appl
75	28	41.2	349	7	US-11-108-528-46	Sequence 46, Appl
76	28	41.2	349	7	US-10-641-678-74	Sequence 74, Appl
77	28	41.2	381	6	US-10-878-556A-149	Sequence 149, App
78	28	41.2	412	6	US-10-821-234-1329	Sequence 5958, Ap
79	28	41.2	644	6	US-10-467-657-1228	Sequence 1228, Ap
80	28	41.2	886	6	US-10-467-657-5408	Sequence 5408, Ap
81	27	39.7	284	6	US-10-714-887-102	Sequence 102, App
82	27	39.7	341	6	US-10-467-657-4417	Sequence 447, App
83	27	39.7	382	7	US-11-117-161-11	Sequence 11, Appl
84	27	39.7	412	7	US-11-080-257-11	Sequence 11, Appl
85	27	39.7	445	6	US-10-858-730-32	Sequence 32, Appl1
86	27	39.7	579	6	US-11-043-590-34	Sequence 34, Appl1
87	26	38.2	168	6	US-10-467-657-2946	Sequence 2946, Ap
88	26	38.2	66	6	US-10-714-887-68	Sequence 68, Appl
89	26	38.2	221	7	US-11-063-343-23	Sequence 23, Appl
90	26	38.2	221	6	US-10-763-312A-115	Sequence 115, App
91	26	38.2	236	6	US-10-714-887-124	Sequence 124, App
92	26	38.2	255	6	US-10-170-997-2	Sequence 2, Appl1
93	26	38.2	255	6	US-11-182-946-11	Sequence 11, Appl1
94	26	38.2	259	6	US-10-631-558-4	Sequence 4, Appl1
95	26	38.2	300	7	US-11-006-119-31	Sequence 31, Appl

99	38.2	329	6	US-10-714-887-116	Sequence 116, App	172	25	36.8	374	7	US-11-037-243-61	Sequence 61, App1
100	38.2	343	7	US-11-074-176-160	Sequence 160, App	173	25	36.8	382	7	US-11-134-795-19	Sequence 17, App1
101	38.2	359	6	US-10-055-877-272	Sequence 272, App	174	25	36.8	396	7	US-11-114-922-75	Sequence 76, App1
102	38.2	361	6	US-10-467-657-7946	Sequence 7946, Ap	175	25	36.8	398	6	US-10-467-657-5642	Sequence 5642, Ap
103	38.2	364	6	US-10-858-730-123	Sequence 123, App	176	25	36.8	401	6	US-10-878-556A-179	Sequence 179, App
104	38.2	394	6	US-10-392-234A-46	Sequence 46, App1	177	25	36.8	405	6	US-10-467-657-2310	Sequence 2310, Ap
105	38.2	394	6	US-10-392-234A-52	Sequence 52, App1	178	25	36.8	423	6	US-10-467-657-6536	Sequence 6536, Ap
106	38.2	412	7	US-11-117-161-13	Sequence 13, App1	179	25	36.8	427	6	US-10-714-887-132	Sequence 132, App
107	38.2	412	7	US-11-080-257-13	Sequence 13, App1	180	25	36.8	433	7	US-11-082-389-132	Sequence 332, App
108	38.2	416	7	US-11-016-706-38	Sequence 38, App1	181	25	36.8	446	7	US-11-082-389-316	Sequence 316, App
109	38.2	464	7	US-11-024-959-488	Sequence 488, App	182	25	36.8	447	6	US-10-967-527A-14	Sequence 14, App1
110	38.2	504	7	US-11-087-100-32	Sequence 32, App1	183	25	36.8	448	6	US-10-967-527A-16	Sequence 16, App1
111	38.2	504	7	US-11-087-084-32	Sequence 32, App1	184	25	36.8	449	6	US-10-821-234-1089	Sequence 1089, Ap
112	38.2	504	7	US-11-087-085-32	Sequence 32, App1	185	25	36.8	460	6	US-10-467-657-3136	Sequence 3136, Ap
113	38.2	510	7	US-11-087-100-26	Sequence 26, App1	186	25	36.8	467	7	US-11-082-389-334	Sequence 334, App
114	38.2	510	7	US-11-087-084-26	Sequence 26, App1	187	25	36.8	472	7	US-11-165-211-1	Sequence 1, App1
115	38.2	510	7	US-11-087-085-26	Sequence 26, App1	188	25	36.8	472	7	US-11-165-211-2	Sequence 2, App1
116	38.2	516	6	US-10-486-968-52	Sequence 52, App1	189	25	36.8	472	7	US-11-165-211-3	Sequence 3, App1
117	38.2	544	6	US-10-980-388-40	Sequence 40, App1	190	25	36.8	472	7	US-11-165-211-4	Sequence 4, App1
118	38.2	592	6	US-10-467-657-4888	Sequence 4888, Ap	191	25	36.8	472	7	US-11-165-226-5	Sequence 5, App1
119	38.2	642	6	US-10-995-561-631	Sequence 631, App	192	25	36.8	472	7	US-11-165-211-7	Sequence 7, App1
120	38.2	657	6	US-10-995-561-622	Sequence 622, App	193	25	36.8	472	7	US-11-165-226-1	Sequence 1, App1
121	38.2	792	7	US-11-108-1172-1127	Sequence 1127, Ap	194	25	36.8	472	7	US-11-165-226-2	Sequence 2, App1
122	38.2	984	6	US-10-995-561-629	Sequence 629, App	195	25	36.8	472	7	US-11-165-226-3	Sequence 3, App1
123	38.2	1076	6	US-10-467-657-5708	Sequence 5708, Ap	196	25	36.8	472	7	US-11-165-226-4	Sequence 4, App1
124	38.2	1289	6	US-10-467-657-334	Sequence 334, App	197	25	36.8	472	7	US-11-165-226-5	Sequence 5, App1
125	38.2	1503	7	US-11-087-100-6	Sequence 6, App1	198	25	36.8	472	7	US-11-165-226-7	Sequence 7, App1
126	38.2	1503	7	US-11-087-084-6	Sequence 6, App1	199	25	36.8	472	7	US-11-165-226-9	Sequence 9, App1
127	38.2	1503	7	US-11-087-085-6	Sequence 6, App1	200	25	36.8	472	7	US-11-165-226-10	Sequence 10, App1
128	38.2	1713	6	US-10-766-317-2	Sequence 2, App1	201	25	36.8	472	7	US-11-165-226-11	Sequence 11, App1
129	38.2	1724	6	US-10-766-317-6	Sequence 6, App1	202	25	36.8	472	7	US-11-165-226-12	Sequence 12, App1
130	38.2	2059	7	US-11-087-100-4	Sequence 4, App1	203	25	36.8	472	7	US-11-165-226-13	Sequence 13, App1
131	38.2	2059	7	US-11-087-084-4	Sequence 4, App1	204	25	36.8	494	6	US-10-467-657-4376	Sequence 4376, Ap
132	38.2	2059	7	US-11-087-085-4	Sequence 4, App1	205	25	36.8	539	6	US-10-467-657-6792	Sequence 6792, Ap
133	38.2	2296	6	US-10-995-561-633	Sequence 633, App	206	25	36.8	567	6	US-10-131-826A-534	Sequence 254, App
134	38.2	2355	6	US-10-995-561-623	Sequence 623, App	207	25	36.8	569	6	US-10-512-184-66	Sequence 66, App1
135	38.2	2355	6	US-10-995-561-627	Sequence 627, App	208	25	36.8	576	6	US-10-512-184-65	Sequence 65, App1
136	38.2	2386	6	US-10-821-234-1545	Sequence 1545, Ap	209	25	36.8	594	6	US-10-467-657-6376	Sequence 6376, Ap
137	38.2	2386	6	US-10-995-561-626	Sequence 626, App	210	25	36.8	607	7	US-11-024-959-381	Sequence 381, App
138	38.2	3333	6	US-10-766-317-4	Sequence 4, App1	211	25	36.8	615	6	US-10-512-184-50	Sequence 50, App1
139	38.2	3507	7	US-11-075-185-7	Sequence 7, App1	212	25	36.8	628	6	US-10-512-184-48	Sequence 48, App1
140	38.2	3712	7	US-11-019-711-48	Sequence 48, App1	213	25	36.8	625	6	US-10-512-184-47	Sequence 47, App1
141	38.2	3712	7	US-11-019-711-51	Sequence 51, App1	214	25	36.8	626	6	US-10-512-184-49	Sequence 49, App1
142	37.5	815	7	US-11-073-112-3	Sequence 3, App1	215	25	36.8	645	7	US-11-154-337-13	Sequence 13, App1
143	36.8	15	7	US-11-033-039-629	Sequence 629, App	216	25	36.8	742	7	US-11-127-877-41	Sequence 43, App1
144	36.8	31	7	US-11-033-039-631	Sequence 631, App	217	25	36.8	765	6	US-10-821-234-1164	Sequence 1164, Ap
145	36.8	45	6	US-10-957-887B-41	Sequence 41, App1	218	25	36.8	1144	6	US-10-467-657-962B-89	Sequence 89, App1
146	36.8	120	7	US-11-116-144-160	Sequence 160, App	219	25	36.8	1255	6	US-10-770-726-62	Sequence 62, App1
147	36.8	120	7	US-11-116-144-161	Sequence 161, App	220	25	36.8	1255	7	US-11-022-562-213	Sequence 213, App
148	36.8	165	5	US-10-878-556A-81	Sequence 81, App1	221	25	36.8	1255	7	US-11-113-202-10	Sequence 10, App1
149	36.8	169	5	US-09-978-360A-443	Sequence 443, App	222	25	36.8	1255	7	US-11-033-039-553	Sequence 553, App
150	36.8	171	6	US-10-467-657-1838	Sequence 1838, Ap	223	25	36.8	1255	7	US-11-135-288-9	Sequence 9, App1
151	36.8	178	6	US-10-821-234-1647	Sequence 1647, Ap	224	25	36.8	1255	7	US-11-202-516-4	Sequence 4, App1
152	36.8	188	6	US-10-467-657-1982	Sequence 1982, Ap	225	25	36.8	1258	7	US-11-033-039-930	Sequence 930, App1
153	36.8	210	6	US-10-467-657-3984	Sequence 3984, Ap	226	25	36.8	2440	6	US-10-766-317-10	Sequence 10, App1
154	36.8	210	6	US-10-055-877-24	Sequence 24, App1	227	25	36.8	2471	7	US-11-050-346-68	Sequence 68, App1
155	36.8	218	7	US-11-082-389-318	Sequence 318, App	228	25	36.8	2556	7	US-11-050-346-67	Sequence 67, App1
156	36.8	234	6	US-10-467-657-7422	Sequence 7422, Ap	229	25	36.8	3500	7	US-11-085-775-2	Sequence 2, App1
157	36.8	236	6	US-11-000-463-278	Sequence 278, App	230	25	36.8	3635	7	US-11-019-711-47	Sequence 47, App1
158	36.8	251	6	US-10-821-234-1470	Sequence 1470, App	231	25	36.0	163	6	US-10-467-657-5884	Sequence 5884, Ap
159	36.8	301	6	US-10-512-184-37	Sequence 37, App1	232	24	35.3	24.5	36.0	US-11-156-843-56	Sequence 56, App1
160	36.8	311	7	US-11-082-389-168	Sequence 168, App	233	24	35.3	30	7	US-11-156-843-94	Sequence 94, App1
161	36.8	316	6	US-10-467-657-4040	Sequence 4040, Ap	234	24	35.3	30	7	US-11-156-843-97	Sequence 97, App1
162	36.8	321	6	US-10-478-345-8	Sequence 8, App1	235	24	35.3	30	7	US-11-156-843-98	Sequence 98, App1
163	36.8	322	6	US-10-055-877-26	Sequence 26, App1	236	24	35.3	49	6	US-10-467-657-4058	Sequence 4058, Ap
164	36.8	325	6	US-10-063-703-64	Sequence 64, App1	237	24	35.3	75	6	US-10-467-657-9139	Sequence 9139, Ap
165	36.8	325	7	US-11-102-240-64	Sequence 64, App1	238	24	35.3	79	7	US-11-077-386-21	Sequence 21, App1
166	36.8	335	7	US-11-152-892-12	Sequence 12, App1	239	24	35.3	124	6	US-10-467-657-3838	Sequence 3838, Ap
167	36.8	344	7	US-11-083-800-10	Sequence 10, App1	240	24	35.3	142	6	US-10-763-712A-117	Sequence 117, App
168	36.8	361	7	US-11-120-308-82	Sequence 82, App1	241	24	35.3	187	7	US-11-205-109-19	Sequence 19, App1
169	36.8	369	6	US-10-793-626-672	Sequence 672, App	242	24	35.3	201	6	US-10-467-657-2006	Sequence 2006, Ap
170	36.8	374	6	US-10-055-877-20	Sequence 20, App1	243	24	35.3	217	6	US-10-467-657-8174	Sequence 8174, Ap
171	36.8	374	6	US-10-055-877-22	Sequence 22, App1	244	24	35.3	220	6	US-10-467-657-8734	Sequence 8734, Ap

245	24	35.3	220	6	US-10-714-887-60	Sequence 60, Appl	318	24	35.3	2551	6	US-10-453-372-256	Sequence 256, App
246	24	35.3	225	6	US-10-467-657-146	Sequence 146, App	319	24	35.3	2551	6	US-11-128-059-96	Sequence 96, Appl
247	24	35.3	225	6	US-10-467-657-4138	Sequence 4138, Ap	320	24	35.3	2766	7	US-10-877-346-62	Sequence 62, Appl
248	24	35.3	225	6	US-10-467-657-7072	Sequence 7072, Ap	321	24	35.3	5179	7	US-11-108-172-1068	Sequence 1068, Ap
249	24	35.3	225	6	US-10-714-887-112	Sequence 112, Appl	322	23.5	34.6	249	7	US-11-054-515-1957	Sequence 1957, Ap
250	24	35.3	242	6	US-10-714-887-66	Sequence 66, Appl	323	23	33.8	21	6	US-10-893-584-205	Sequence 205, App
251	24	35.3	254	6	US-10-467-657-3450	Sequence 3450, Ap	324	23	33.8	24	6	US-10-467-657-9084	Sequence 9084, Ap
252	24	35.3	279	6	US-10-055-877-197	Sequence 197, App	325	23	33.8	83	7	US-11-082-389-158	Sequence 158, App
253	24	35.3	279	6	US-10-714-887-58	Sequence 58, Appl	326	23	33.8	85	6	US-10-467-657-7338	Sequence 7438, Ap
254	24	35.3	284	6	US-10-467-657-536	Sequence 536, App	327	23	33.8	86	6	US-10-485-788A-822	Sequence 822, App
255	24	35.3	297	6	US-10-510-386-16	Sequence 16, Appl	328	23	33.8	86	7	US-11-053-076-207	Sequence 207, App
256	24	35.3	312	6	US-10-714-887-44	Sequence 44, Appl	329	23	33.8	89	6	US-10-467-657-3582	Sequence 3582, Ap
257	24	35.3	323	7	US-11-120-308-108	Sequence 108, App	330	23	33.8	110	6	US-10-793-626-930	Sequence 930, App
258	24	35.3	323	7	US-11-120-308-116	Sequence 116, App	331	23	33.8	119	6	US-10-467-657-6638	Sequence 6638, Ap
259	24	35.3	339	6	US-10-467-657-4318	Sequence 4318, Ap	332	23	33.8	122	7	US-11-116-144-164	Sequence 164, App
260	24	35.3	360	7	US-11-108-528-8	Sequence 8, Appl	333	23	33.8	133	6	US-10-793-626-2072	Sequence 2072, Ap
261	24	35.3	363	7	US-11-111-239-6	Sequence 6, Appl	334	23	33.8	160	7	US-11-044-285-4	Sequence 4, Appl
262	24	35.3	386	6	US-10-858-730-236	Sequence 236, App	335	23	33.8	163	6	US-10-467-657-4786	Sequence 4786, Ap
263	24	35.3	393	7	US-11-111-239-8	Sequence 8, Appl	336	23	33.8	181	6	US-10-793-626-560	Sequence 560, App
264	24	35.3	396	6	US-10-510-386-238	Sequence 238, App	337	23	33.8	199	6	US-10-793-626-2832	Sequence 2832, Ap
265	24	35.3	399	6	US-10-510-386-30	Sequence 30, Appl	338	23	33.8	221	6	US-10-821-224-1139	Sequence 1139, Ap
266	24	35.3	399	7	US-11-111-239-10	Sequence 10, Appl	339	23	33.8	224	7	US-10-467-657-5140	Sequence 5140, Ap
267	24	35.3	400	6	US-10-467-657-7588	Sequence 7588, Ap	340	23	33.8	226	7	US-11-151-601-37	Sequence 37, Appl
268	24	35.3	410	6	US-11-120-308-114	Sequence 114, App	341	23	33.8	226	7	US-11-151-601-37	Sequence 37, Appl
269	24	35.3	413	7	US-11-043-889-18	Sequence 18, Appl	342	23	33.8	226	7	US-10-131-826A-178	Sequence 178, App
270	24	35.3	417	6	US-10-793-626-196	Sequence 196, App	343	23	33.8	229	6	US-10-467-657-9008	Sequence 9008, Ap
271	24	35.3	427	7	US-11-110-851-66	Sequence 66, Appl	344	23	33.8	238	6	US-10-467-657-4954	Sequence 4954, Ap
272	24	35.3	436	6	US-10-517-939-10	Sequence 10, Appl	345	23	33.8	240	7	US-11-212-443-139	Sequence 139, App
273	24	35.3	436	6	US-11-043-889-58	Sequence 58, Appl	346	23	33.8	241	6	US-10-467-657-1400	Sequence 1400, Ap
274	24	35.3	438	7	US-11-043-889-55	Sequence 55, Appl	347	23	33.8	242	6	US-10-714-887-50	Sequence 50, Appl
275	24	35.3	447	7	US-11-124-368A-185	Sequence 185, App	348	23	33.8	243	7	US-11-129-104-91	Sequence 91, Appl
276	24	35.3	449	6	US-10-878-556A-57	Sequence 57, Appl	349	23	33.8	271	6	US-10-714-887-48	Sequence 48, Appl
277	24	35.3	455	6	US-10-467-657-5828	Sequence 5828, Ap	350	23	33.8	278	6	US-10-467-657-1848	Sequence 1848, Ap
278	24	35.3	465	6	US-10-467-657-5828	Sequence 5828, Ap	351	23	33.8	301	6	US-10-793-626-1396	Sequence 1396, Ap
279	24	35.3	484	7	US-11-147-725-2	Sequence 2, Appl	352	23	33.8	302	6	US-10-793-626-2170	Sequence 2170, Ap
280	24	35.3	505	6	US-10-793-626-2320	Sequence 2220, Ap	353	23	33.8	312	7	US-11-054-281-32	Sequence 32, Appl
281	24	35.3	514	6	US-10-957-569-48	Sequence 48, Appl	354	23	33.8	312	7	US-11-054-281-320	Sequence 320, App
282	24	35.3	516	6	US-10-995-561-559	Sequence 559, App	355	23	33.8	312	7	US-11-109-528-32	Sequence 32, Appl
283	24	35.3	533	7	US-11-128-059-58	Sequence 58, Appl	356	23	33.8	318	7	US-11-109-528-32	Sequence 32, Appl
284	24	35.3	554	7	US-11-159-902-4	Sequence 4, Appl	357	23	33.8	318	7	US-11-109-528-32	Sequence 32, Appl
285	24	35.3	556	6	US-10-063-703-24	Sequence 24, Appl	358	23	33.8	318	7	US-11-111-239-2	Sequence 2, Appl
286	24	35.3	556	6	US-11-102-240-24	Sequence 24, Appl	359	23	33.8	321	6	US-10-467-657-2504	Sequence 2504, Ap
287	24	35.3	557	6	US-10-512-109-9	Sequence 9, Appl	360	23	33.8	330	7	US-11-152-882-10	Sequence 10, Appl
288	24	35.3	558	6	US-10-512-109-11	Sequence 11, Appl	361	23	33.8	333	6	US-10-878-556A-174	Sequence 174, App
289	24	35.3	585	7	US-11-012-762-6	Sequence 6, Appl	362	23	33.8	338	6	US-10-467-657-3178	Sequence 3178, Ap
290	24	35.3	613	6	US-10-517-939-298	Sequence 298, App	363	23	33.8	340	6	US-10-055-554A-43	Sequence 43, Appl
291	24	35.3	651	7	US-11-124-368A-184	Sequence 184, App	364	23	33.8	354	6	US-10-467-657-7260	Sequence 7260, Ap
292	24	35.3	672	6	US-10-467-657-8280	Sequence 8280, Ap	365	23	33.8	357	7	US-11-165-466-2	Sequence 2, Appl
293	24	35.3	770	7	US-11-070-627-8	Sequence 8, Appl	366	23	33.8	357	7	US-11-165-466-2	Sequence 2, Appl
294	24	35.3	770	7	US-11-070-627-10	Sequence 10, Appl	367	23	33.8	359	7	US-11-108-528-32	Sequence 32, Appl
295	24	35.3	774	7	US-11-070-627-7	Sequence 7, Appl	368	23	33.8	360	7	US-11-108-528-32	Sequence 32, Appl
296	24	35.3	833	7	US-11-159-902-2	Sequence 2, Appl	369	23	33.8	361	7	US-11-108-528-32	Sequence 32, Appl
297	24	35.3	884	6	US-10-995-561-786	Sequence 786, App	370	23	33.8	363	7	US-11-052-554A-169	Sequence 169, App
298	24	35.3	911	6	US-10-858-730-9	Sequence 9, Appl	371	23	33.8	363	7	US-11-054-281-120	Sequence 120, App
299	24	35.3	921	6	US-11-183-624-2	Sequence 2, Appl	372	23	33.8	365	6	US-10-624-932-24	Sequence 24, Appl
300	24	35.3	1023	6	US-10-995-561-968	Sequence 968, App	373	23	33.8	372	7	US-11-108-528-10	Sequence 10, Appl
301	24	35.3	1076	6	US-10-131-826A-119	Sequence 219, App	374	23	33.8	372	7	US-11-108-528-10	Sequence 10, Appl
302	24	35.3	1125	7	US-11-024-959-360	Sequence 360, App	375	23	33.8	377	6	US-10-467-657-7508	Sequence 7508, Ap
303	24	35.3	1416	7	US-11-128-059-60	Sequence 60, App	376	23	33.8	380	6	US-10-624-932-10	Sequence 20, Appl
304	24	35.3	1494	7	US-11-128-059-78	Sequence 78, Appl	377	23	33.8	380	6	US-10-624-932-22	Sequence 22, Appl
305	24	35.3	1532	6	US-10-821-234-914	Sequence 914, App	378	23	33.8	380	6	US-11-108-528-30	Sequence 28, Appl
306	24	35.3	1765	6	US-10-055-877-140	Sequence 140, App	379	23	33.8	380	7	US-11-108-528-30	Sequence 30, Appl
307	24	35.3	1940	6	US-10-055-877-141	Sequence 141, App	380	23	33.8	384	6	US-10-467-657-5664	Sequence 5664, Ap
308	24	35.3	2086	7	US-11-128-059-82	Sequence 82, Appl	381	23	33.8	384	7	US-11-129-133-77	Sequence 77, Appl
309	24	35.3	2098	6	US-10-055-877-253	Sequence 253, App	382	23	33.8	389	6	US-10-821-234-1401	Sequence 1401, Ap
310	24	35.3	2313	7	US-11-128-059-80	Sequence 80, Appl	383	23	33.8	389	7	US-11-108-528-14	Sequence 14, Appl
311	24	35.3	2358	7	US-11-128-059-74	Sequence 74, Appl	384	23	33.8	391	7	US-11-108-528-12	Sequence 12, Appl
312	24	35.3	2417	6	US-10-453-372-228	Sequence 228, App	385	23	33.8	413	7	US-11-052-554A-308	Sequence 308, App
313	24	35.3	2439	7	US-11-128-059-76	Sequence 76, Appl	386	23	33.8	425	6	US-10-858-730-3	Sequence 3, Appl
314	24	35.3	2459	7	US-11-128-059-94	Sequence 94, Appl	387	23	33.8	435	6	US-10-467-657-4570	Sequence 4570, Ap
315	24	35.3	2491	6	US-10-995-561-769	Sequence 769, App	388	23	33.8	473	7	US-11-040-595-9	Sequence 9, Appl
316	24	35.3	2505	7	US-11-126-313-33	Sequence 33, Appl	389	23	33.8	474	7	US-11-040-595-8	Sequence 8, Appl
317	24	35.3					390	23	33.8	480	7	US-11-080-991-76	Sequence 76, Appl

331	23	33.8	487	7	US-11-040-595-6	Sequence 6, Appl	464	22	33.4	15	7	US-11-188-552-29	Sequence 29, Appl
332	23	33.8	490	6	US-10-131-825A-356	Sequence 356, App	465	22	33.4	17	6	US-11-063-186-60	Sequence 39, Appl
333	23	33.8	494	7	US-11-165-697-48	Sequence 48, Appl	466	22	33.4	18	6	US-10-763-286A-39	Sequence 39, Appl
334	23	33.8	494	7	US-11-165-697-49	Sequence 49, Appl	467	22	33.4	23	6	US-10-893-584-268	Sequence 268, App
335	23	33.8	500	7	US-11-120-308-138	Sequence 138, App	468	22	33.4	26	7	US-11-114-813-4	Sequence 4, Appl1
336	23	33.8	505	6	US-10-467-657-5148	Sequence 5148, Ap	469	22	33.4	26	7	US-11-115-003-4	Sequence 4, Appl1
337	23	33.8	508	6	US-10-467-657-7826	Sequence 7826, Ap	470	22	33.4	27	6	US-10-893-584-254	Sequence 254, App
338	23	33.8	518	6	US-10-821-234-1165	Sequence 1165, Ap	471	22	33.4	29	6	US-10-893-584-219	Sequence 219, App
339	23	33.8	525	6	US-10-763-712A-108	Sequence 108, App	472	22	33.4	30	7	US-11-156-843-59	Sequence 59, Appl
400	23	33.8	525	7	US-11-082-389-36	Sequence 389-36	473	22	33.4	30	7	US-11-156-843-62	Sequence 62, Appl
401	23	33.8	542	7	US-11-019-711-97	Sequence 97, Appl	474	22	33.4	30	7	US-11-156-843-64	Sequence 64, Appl
402	23	33.8	545	7	US-11-082-389-34	Sequence 34, Appl	475	22	33.4	30	7	US-11-156-843-67	Sequence 67, Appl
403	23	33.8	547	7	US-11-082-389-86	Sequence 86, Appl	476	22	33.4	30	7	US-11-156-843-73	Sequence 73, Appl
404	23	33.8	550	6	US-10-878-556A-166	Sequence 166, App	477	22	33.4	30	7	US-11-156-843-76	Sequence 76, Appl
405	23	33.8	560	6	US-11-205-109-38	Sequence 38, Appl	478	22	33.4	30	7	US-11-156-843-78	Sequence 78, Appl
406	23	33.8	561	6	US-10-454-437-330	Sequence 330, App	479	22	33.4	30	7	US-11-156-843-81	Sequence 81, Appl
407	23	33.8	575	6	US-10-980-388-46	Sequence 46, Appl	480	22	33.4	30	7	US-11-156-843-87	Sequence 87, Appl
408	23	33.8	579	6	US-11-045-802-33	Sequence 33, Appl	481	22	33.4	30	7	US-11-156-843-88	Sequence 88, Appl
409	23	33.8	601	6	US-10-467-657-7120	Sequence 7120, Ap	482	22	33.4	30	7	US-11-156-843-90	Sequence 90, Appl
410	23	33.8	608	7	US-11-024-959-481	Sequence 481, App	483	22	33.4	30	7	US-11-156-843-91	Sequence 91, Appl
411	23	33.8	611	7	US-11-082-389-436	Sequence 436, App	484	22	33.4	30	7	US-11-156-843-92	Sequence 92, Appl
412	23	33.8	644	7	US-11-024-959-502	Sequence 502, App	485	22	33.4	30	7	US-11-156-843-93	Sequence 93, Appl
413	23	33.8	654	7	US-11-184-860-1	Sequence 1, Appl1	486	22	33.4	30	7	US-11-156-843-95	Sequence 95, Appl
414	23	33.8	655	7	US-11-124-368A-296	Sequence 296, App	487	22	33.4	30	7	US-11-156-843-96	Sequence 96, Appl
415	23	33.8	655	7	US-11-124-368A-297	Sequence 297, App	488	22	33.4	40	6	US-10-467-657-7558	Sequence 7558, Ap
416	23	33.8	665	7	US-11-113-837-19	Sequence 19, Appl	489	22	33.4	43	6	US-10-467-657-5420	Sequence 5420, Ap
417	23	33.8	709	7	US-11-165-067A-9	Sequence 9, Appl1	490	22	33.4	97	6	US-10-485-788A-756	Sequence 756, App
418	23	33.8	717	6	US-10-467-657-8056	Sequence 8056, Ap	491	22	33.4	97	6	US-11-053-076-133	Sequence 133, App
419	23	33.8	732	6	US-10-467-657-5888	Sequence 5888, Ap	492	22	33.4	97	7	US-11-075-351-59	Sequence 59, Appl
420	23	33.8	879	6	US-10-858-730-10	Sequence 10, Appl	493	22	33.4	113	6	US-10-746-609-11	Sequence 11, Appl
421	23	33.8	883	6	US-10-858-730-207	Sequence 207, App	494	22	33.4	119	6	US-10-793-626-424	Sequence 424, App
422	23	33.8	897	6	US-10-356-263A-58	Sequence 58, Appl	495	22	33.4	138	6	US-10-467-657-5374	Sequence 5374, Ap
423	23	33.8	914	7	US-11-052-554A-160	Sequence 160, App	496	22	33.4	140	7	US-11-054-281-117	Sequence 117, App
424	23	33.8	930	6	US-10-821-234-1188	Sequence 1188, Ap	497	22	33.4	140	7	US-10-793-626-1170	Sequence 1170, App
425	23	33.8	1059	6	US-10-336-263A-54	Sequence 54, Appl	498	22	33.4	153	6	US-10-467-657-4112	Sequence 4112, Ap
426	23	33.8	1059	6	US-10-336-263A-56	Sequence 56, Appl	499	22	33.4	157	6	US-10-793-626-1120	Sequence 1120, Ap
427	23	33.8	1210	7	US-11-108-172-692	Sequence 692, App	500	22	33.4	171	7	US-11-055-882-352	Sequence 352, App
428	23	33.8	1236	6	US-10-873-528-109	Sequence 109, App	501	22	33.4	178	6	US-10-467-657-3862	Sequence 3862, Ap
429	23	33.8	1403	6	US-10-055-877-52	Sequence 52, Appl	502	22	33.4	179	6	US-10-923-022-2	Sequence 2, Appl1
430	23	33.8	1403	6	US-10-453-372-878	Sequence 878, Appl	503	22	33.4	185	6	US-10-467-657-144	Sequence 144, App
431	23	33.8	1404	6	US-10-055-877-44	Sequence 44, Appl	504	22	33.4	185	6	US-10-467-657-4092	Sequence 4092, Ap
432	23	33.8	1404	6	US-10-453-372-870	Sequence 870, App	505	22	33.4	185	6	US-10-467-657-7068	Sequence 7068, Ap
433	23	33.8	1547	6	US-10-453-372-886	Sequence 886, App	506	22	33.4	185	6	US-10-923-022-9	Sequence 9, Appl1
434	23	33.8	1548	7	US-11-108-172-1095	Sequence 1095, Ap	507	22	33.4	187	5	US-09-978-360A-758	Sequence 758, App
435	23	33.8	1577	6	US-10-055-877-54	Sequence 54, Appl	508	22	33.4	188	6	US-10-923-022-4	Sequence 4, Appl1
436	23	33.8	1577	6	US-10-453-372-882	Sequence 882, App	509	22	33.4	188	6	US-10-923-022-8	Sequence 8, Appl1
437	23	33.8	1577	6	US-10-453-372-884	Sequence 884, App	510	22	33.4	188	7	US-11-000-463-460	Sequence 460, App
438	23	33.8	1618	6	US-10-984-645-2	Sequence 2, Appl1	511	22	33.4	188	7	US-11-000-463-932	Sequence 932, App
439	23	33.8	1620	6	US-10-453-372-868	Sequence 868, App	512	22	33.4	189	6	US-10-923-022-6	Sequence 6, Appl1
440	23	33.8	1653	6	US-10-453-372-866	Sequence 866, App	513	22	33.4	190	6	US-10-923-022-11	Sequence 11, Appl
441	23	33.8	1725	6	US-10-766-317-8	Sequence 8, Appl1	514	22	33.4	191	6	US-10-467-657-818	Sequence 818, App
442	23	33.8	1804	6	US-10-513-786-2	Sequence 2, Appl1	515	22	33.4	198	6	US-10-923-022-3	Sequence 3, Appl1
443	23	33.8	1873	7	US-11-126-313-29	Sequence 29, Appl	516	22	33.4	198	6	US-10-923-022-5	Sequence 5, Appl1
444	23	33.8	1892	7	US-11-075-185-6	Sequence 6, Appl1	517	22	33.4	199	6	US-10-923-022-7	Sequence 7, Appl1
445	23	33.8	1992	7	US-11-013-759-3	Sequence 13, Appl	518	22	33.4	200	6	US-10-454-437-246	Sequence 246, App
446	23	33.8	1992	7	US-11-013-759-13	Sequence 13, Appl	519	22	33.4	200	6	US-10-923-022-10	Sequence 10, Appl
447	23	33.8	2047	7	US-11-013-759-4	Sequence 4, Appl1	520	22	33.4	203	6	US-10-467-657-13100	Sequence 3100, Ap
448	23	33.8	2047	7	US-11-013-759-7	Sequence 7, Appl1	521	22	33.4	204	6	US-10-467-657-4830	Sequence 4830, Ap
449	23	33.8	2214	7	US-11-013-759-11	Sequence 11, Appl	522	22	33.4	205	7	US-11-165-067A-47	Sequence 47, Appl
450	23	33.8	2890	7	US-11-115-639-31	Sequence 31, Appl	523	22	33.4	212	6	US-10-982-545-7	Sequence 7, Appl1
451	23	33.8	2890	7	US-11-115-639-32	Sequence 32, Appl	524	22	33.4	225	7	US-11-082-389-146	Sequence 146, App
452	23	33.8	2890	7	US-11-115-639-33	Sequence 33, Appl	525	22	33.4	228	6	US-10-980-388-17	Sequence 17, Appl
453	23	33.8	2897	7	US-11-019-711-6	Sequence 6, Appl1	526	22	33.4	237	6	US-10-714-887-104	Sequence 104, App
454	23	33.8	3600	7	US-11-019-711-2	Sequence 2, Appl1	527	22	33.4	244	6	US-10-793-626-2780	Sequence 2780, App
455	23	33.8	3655	7	US-11-075-185-5	Sequence 5, Appl1	528	22	33.4	255	6	US-10-485-517-360	Sequence 360, App
456	23	33.8	3690	6	US-10-995-561-1016	Sequence 1016, Ap	529	22	33.4	256	6	US-11-179-977-15	Sequence 15, Appl
457	23	33.8	3704	6	US-10-513-786-1	Sequence 1, Appl1	530	22	33.4	261	6	US-10-763-712A-113	Sequence 113, App
458	23	33.8	3714	6	US-10-995-561-1015	Sequence 1015, Ap	531	22	33.4	263	7	US-11-134-795-12	Sequence 12, App
459	23	33.8	3717	6	US-10-821-234-1076	Sequence 1076, Ap	532	22	33.4	263	7	US-11-082-389-144	Sequence 144, App
460	23	33.8	8695	7	US-11-205-109-15	Sequence 15, Appl	533	22	33.4	264	6	US-10-714-887-108	Sequence 108, App
461	23	32.4	8	7	US-11-047-383-15	Sequence 15, Appl	534	22	33.4	268	7	US-11-014-887-24	Sequence 24, Appl
462	22	32.4	13	7	US-11-047-383-27	Sequence 27, Appl	535	22	33.4	279	6	US-10-467-657-13110	Sequence 1310, Ap
463	22	32.4	14	7	US-11-188-552-42	Sequence 42, Appl	536	22	33.4	279	7	US-11-102-497-8	Sequence 8, Appl1

537	22	32.4	284	6	US-10-467-657-3920	Sequence 3920, Ap	610	22	32.4	495	7	US-11-052-554A-258	Sequence 258, App
538	22	32.4	290	6	US-10-714-887-110	Sequence 110, App	611	22	32.4	500	6	US-10-517-939-114	Sequence 174, App
539	22	32.4	294	7	US-11-143-980-36	Sequence 36, Appl	612	22	32.4	507	6	US-10-454-437-38	Sequence 38, Appl
540	22	32.4	296	6	US-10-467-657-5502	Sequence 5502, Ap	613	22	32.4	513	7	US-11-149-349-6	Sequence 6, Appl
541	22	32.4	300	6	US-10-667-295-117	Sequence 117, App	614	22	32.4	522	7	US-11-054-281-145	Sequence 124, App
542	22	32.4	302	6	US-10-667-295-116	Sequence 116, App	615	22	32.4	522	7	US-11-054-281-135	Sequence 125, App
543	22	32.4	307	6	US-10-467-657-7006	Sequence 7006, Ap	616	22	32.4	523	6	US-10-453-377-1006	Sequence 1006, Ap
544	22	32.4	310	6	US-11-055-163-9	Sequence 9, Appl	617	22	32.4	523	6	US-10-453-377-1008	Sequence 1008, Ap
545	22	32.4	312	6	US-10-714-887-54	Sequence 54, Appl	618	22	32.4	523	7	US-11-054-281-122	Sequence 122, App
546	22	32.4	316	6	US-10-667-295-115	Sequence 115, App	619	22	32.4	523	7	US-11-054-281-123	Sequence 123, App
547	22	32.4	317	6	US-10-485-517-196	Sequence 196, App	620	22	32.4	541	7	US-11-010-239-95	Sequence 95, Appl
548	22	32.4	319	7	US-11-184-005-8	Sequence 8, Appl	621	22	32.4	574	6	US-10-527-771-14	Sequence 14, Appl
549	22	32.4	325	7	US-11-184-005-4	Sequence 4, Appl	622	22	32.4	576	6	US-10-923-022-1	Sequence 1, Appl
550	22	32.4	327	7	US-11-024-959-455	Sequence 455, App	623	22	32.4	599	6	US-10-467-657-3972	Sequence 3972, Ap
551	22	32.4	333	7	US-11-004-789-2	Sequence 2, Appl	624	22	32.4	608	7	US-11-109-157A-11	Sequence 11, Appl
552	22	32.4	334	6	US-10-714-887-46	Sequence 46, Appl	625	22	32.4	619	7	US-11-109-157A-42	Sequence 42, Appl
553	22	32.4	334	7	US-11-111-239-4	Sequence 4, Appl	626	22	32.4	630	6	US-10-893-584-274	Sequence 274, App
554	22	32.4	334	7	US-11-127-817-14	Sequence 14, Appl	627	22	32.4	641	7	US-11-094-519A-29	Sequence 29, Appl
555	22	32.4	336	7	US-11-127-877-69	Sequence 69, Appl	628	22	32.4	655	7	US-11-045-802-29	Sequence 29, Appl
556	22	32.4	336	6	US-10-454-437-230	Sequence 230, App	629	22	32.4	664	6	US-10-821-234-1670	Sequence 1670, Ap
557	22	32.4	344	7	US-11-055-163-8	Sequence 8, Appl	630	22	32.4	664	6	US-10-995-561-964	Sequence 964, App
558	22	32.4	360	7	US-11-112-240-1	Sequence 1, Appl	631	22	32.4	664	6	US-10-995-561-965	Sequence 965, App
559	22	32.4	360	7	US-11-112-304A-1	Sequence 1, Appl	632	22	32.4	674	6	US-10-821-234-965	Sequence 965, App
560	22	32.4	361	6	US-10-838-616-6	Sequence 6, Appl	633	22	32.4	690	6	US-10-131-826A-106	Sequence 306, App
561	22	32.4	363	7	US-11-074-176-296	Sequence 296, App	634	22	32.4	693	6	US-10-131-826A-406	Sequence 406, App
562	22	32.4	372	6	US-10-714-887-114	Sequence 114, App	635	22	32.4	708	6	US-10-131-826A-298	Sequence 298, App
563	22	32.4	376	7	US-11-109-157A-12	Sequence 12, Appl	636	22	32.4	713	6	US-10-453-372-48	Sequence 48, Appl
564	22	32.4	377	6	US-10-525-674-22	Sequence 22, Appl	637	22	32.4	725	6	US-10-467-657-1536	Sequence 1536, Ap
565	22	32.4	377	7	US-11-055-822-448	Sequence 448, App	638	22	32.4	728	7	US-11-053-100-54	Sequence 54, Appl
566	22	32.4	379	7	US-11-055-822-446	Sequence 446, App	639	22	32.4	729	7	US-11-210-316-29	Sequence 29, Appl
567	22	32.4	387	7	US-11-092-140-17	Sequence 17, Appl	640	22	32.4	730	6	US-10-821-234-1019	Sequence 1019, Ap
568	22	32.4	392	6	US-10-392-234A-50	Sequence 50, Appl	641	22	32.4	776	6	US-10-453-372-44	Sequence 44, Appl
569	22	32.4	392	6	US-10-873-528-142	Sequence 142, App	642	22	32.4	776	6	US-10-453-372-46	Sequence 46, Appl
570	22	32.4	393	6	US-10-467-657-1038	Sequence 1038, Ap	643	22	32.4	783	7	US-11-186-284-59	Sequence 59, Appl
571	22	32.4	394	6	US-10-131-826A-520	Sequence 520, App	644	22	32.4	784	6	US-10-517-939-334	Sequence 324, App
572	22	32.4	395	7	US-11-075-185-13	Sequence 13, Appl	645	22	32.4	787	6	US-10-517-939-54	Sequence 54, Appl
573	22	32.4	397	6	US-10-641-678-32	Sequence 32, Appl	646	22	32.4	795	7	US-11-109-157A-14	Sequence 14, Appl
574	22	32.4	400	6	US-10-467-657-2702	Sequence 2702, Ap	647	22	32.4	801	6	US-10-467-657-1670	Sequence 6470, Ap
575	22	32.4	402	6	US-10-793-626-2282	Sequence 2282, Ap	648	22	32.4	801	6	US-10-467-657-1866	Sequence 1866, Ap
576	22	32.4	416	6	US-10-641-678-73	Sequence 73, Appl	649	22	32.4	817	7	US-11-109-157A-10	Sequence 10, Appl
577	22	32.4	419	6	US-10-979-821-4	Sequence 4, Appl	650	22	32.4	879	7	US-11-053-100-55	Sequence 55, Appl
578	22	32.4	419	6	US-10-979-821-6	Sequence 6, Appl	651	22	32.4	879	7	US-11-053-100-57	Sequence 57, Appl
579	22	32.4	419	7	US-11-114-922-4	Sequence 4, Appl	652	22	32.4	882	6	US-10-453-372-58	Sequence 58, Appl
580	22	32.4	419	7	US-11-114-922-6	Sequence 6, Appl	653	22	32.4	884	6	US-10-453-372-58	Sequence 58, Appl
581	22	32.4	421	6	US-10-667-974-2	Sequence 2, Appl	654	22	32.4	896	7	US-11-192-219-3	Sequence 3, Appl
582	22	32.4	421	6	US-10-858-730-1	Sequence 1, Appl	655	22	32.4	896	7	US-11-166-720-3	Sequence 12, Appl
583	22	32.4	421	6	US-10-858-730-202	Sequence 202, App	656	22	32.4	912	6	US-10-964-313-12	Sequence 12, Appl
584	22	32.4	421	6	US-10-525-710-73	Sequence 65, Appl	658	22	32.4	923	7	US-11-192-219-4	Sequence 4, Appl
585	22	32.4	421	6	US-10-525-674-65	Sequence 26, Appl	659	22	32.4	1034	7	US-11-103-957-11	Sequence 11, Appl
586	22	32.4	431	6	US-11-055-822-26	Sequence 26, Appl	660	22	32.4	1065	7	US-11-191-374-16	Sequence 16, Appl
587	22	32.4	431	6	US-10-793-626-2566	Sequence 2566, Ap	661	22	32.4	1065	7	US-11-191-375-16	Sequence 16, Appl
588	22	32.4	433	7	US-11-047-383-2	Sequence 2, Appl	662	22	32.4	1065	7	US-11-191-375-17	Sequence 17, Appl
589	22	32.4	433	7	US-11-047-383-4	Sequence 4, Appl	663	22	32.4	1068	7	US-11-191-374-45	Sequence 45, Appl
590	22	32.4	437	7	US-11-043-542-22	Sequence 22, Appl	664	22	32.4	1068	7	US-11-191-375-45	Sequence 45, Appl
591	22	32.4	438	7	US-11-024-959-342	Sequence 342, App	665	22	32.4	1068	7	US-11-191-375-45	Sequence 45, Appl
592	22	32.4	447	6	US-10-467-657-4034	Sequence 4034, App	666	22	32.4	1069	7	US-11-191-374-17	Sequence 17, Appl
593	22	32.4	447	6	US-10-467-657-7050	Sequence 7050, Ap	667	22	32.4	1069	7	US-11-191-375-17	Sequence 17, Appl
594	22	32.4	456	7	US-11-074-176-238	Sequence 238, App	668	22	32.4	1069	7	US-11-191-375-17	Sequence 17, Appl
595	22	32.4	461	6	US-10-509-464-7	Sequence 7, Appl	669	22	32.4	1072	7	US-11-109-157A-13	Sequence 13, Appl
596	22	32.4	461	7	US-11-082-389-176	Sequence 176, App	670	22	32.4	1103	7	US-11-109-157A-92	Sequence 9, Appl
597	22	32.4	467	6	US-10-467-657-5552	Sequence 5552, Ap	671	22	32.4	1165	7	US-11-192-219-2	Sequence 2, Appl
598	22	32.4	472	7	US-11-165-211-6	Sequence 6, Appl	672	22	32.4	1224	6	US-10-509-565A-2	Sequence 2, Appl
599	22	32.4	472	7	US-11-165-226-6	Sequence 6, Appl	673	22	32.4	1274	6	US-10-454-437-360	Sequence 360, App
600	22	32.4	473	6	US-10-509-464-5	Sequence 5, Appl	674	22	32.4	1329	7	US-11-053-100-56	Sequence 56, Appl
601	22	32.4	473	6	US-10-509-464-6	Sequence 6, Appl	675	22	32.4	1554	7	US-11-186-284-93	Sequence 93, Appl
602	22	32.4	474	6	US-11-037-829A-13	Sequence 13, Appl	676	22	32.4	1587	7	US-11-052-554A-280	Sequence 280, App
603	22	32.4	475	6	US-10-509-464-8	Sequence 8, Appl	677	22	32.4	1857	6	US-10-055-877-252	Sequence 252, App
604	22	32.4	475	6	US-10-467-657-5382	Sequence 5382, Ap	678	22	32.4	2084	6	US-10-055-877-73	Sequence 73, Appl
605	22	32.4	475	6	US-10-467-657-7376	Sequence 7376, Ap	679	22	32.4	2107	6	US-10-995-551-827	Sequence 827, App
606	22	32.4	484	6	US-11-052-554A-170	Sequence 170, App	680	22	32.4	2109	6	US-10-055-877-251	Sequence 251, App
607	22	32.4	485	6	US-10-793-626-1346	Sequence 1346, Ap	681	22	32.4	2143	6	US-10-453-372-1188	Sequence 1188, Ap
608	22	32.4	487	7	US-11-076-733-15	Sequence 15, Appl	682	22	32.4	2314	7	US-11-097-728-2	Sequence 2, Appl
609	22	32.4	488	6	US-10-467-657-6264	Sequence 6264, Ap							

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684	22	31.4	2480	6	US-10-995-561-825	Sequence 825, App	757	21	30.9	63	7	US-11-008-570-100	Sequence 100, App
685	22	32.4	2612	6	US-10-453-372-38	Sequence 38, Appl	758	21	30.9	68	6	US-10-467-657-4860	Sequence 4860, Ap
686	22	33.4	2669	6	US-10-453-372-36	Sequence 36, Appl	759	21	30.9	69	6	US-10-467-657-1212	Sequence 1212, Ap
687	22	33.4	3104	6	US-10-453-372-34	Sequence 34, Appl	760	21	30.9	76	7	US-11-000-463-318	Sequence 318, App
688	22	32.4	3104	6	US-10-453-372-62	Sequence 62, Appl	761	21	30.9	76	7	US-11-000-463-790	Sequence 790, App
689	22	32.4	3104	6	US-10-453-372-64	Sequence 64, Appl	762	21	30.9	78	6	US-10-467-657-1782	Sequence 1782, Ap
690	22	32.4	3116	6	US-10-995-561-826	Sequence 826, App	763	21	30.9	80	7	US-11-226-325-131	Sequence 131, App
691	22	32.4	3130	6	US-10-453-372-42	Sequence 42, App	764	21	30.9	80	7	US-11-226-325-132	Sequence 132, App
692	22	33.4	3194	7	US-11-052-554A-90	Sequence 90, Appl	765	21	30.9	82	7	US-11-166-412-113	Sequence 113, App
693	22	32.4	3483	6	US-10-453-372-40	Sequence 40, Appl	766	21	30.9	80	7	US-11-055-822-456	Sequence 456, App
694	22	32.4	3546	6	US-10-453-372-32	Sequence 32, Appl	767	21	30.9	83	6	US-10-467-657-7926	Sequence 7926, Ap
695	22	32.4	3567	6	US-10-453-372-1112	Sequence 1112, Ap	768	21	30.9	87	6	US-10-839-799-9162	Sequence 112, App
696	22	32.4	3689	7	US-11-075-185-4	Sequence 4, Appli	769	21	30.9	88	7	US-11-194-880-1	Sequence 1, Appli
697	22	32.4	4868	7	US-11-044-111-24	Sequence 24, Appl	770	21	30.9	91	5	US-09-978-360A-801	Sequence 801, App
698	21.5	31.6	35	7	US-11-121-301-8	Sequence 8, Appli	771	21	30.9	95	7	US-11-198-847-227	Sequence 227, App
699	21.5	31.6	152	7	US-11-034-569-4	Sequence 4, Appli	772	21	30.9	95	7	US-11-008-570-118	Sequence 118, App
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701	21.5	31.6	208	6	US-10-467-657-7482	Sequence 7482, Ap	774	21	30.9	97	6	US-10-467-657-4214	Sequence 4214, Ap
702	21.5	31.6	258	7	US-11-090-439-38	Sequence 38, Appl	775	21	30.9	98	6	US-10-530-253-36	Sequence 36, Appl
703	21.5	31.6	321	6	US-10-467-657-1710	Sequence 1710, Ap	776	21	30.9	99	6	US-10-467-657-7214	Sequence 7214, Ap
704	21.5	31.6	442	6	US-10-877-346-21	Sequence 21, Appl	777	21	30.9	100	6	US-10-467-657-1518	Sequence 9162, Ap
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706	21.5	31.6	525	6	US-10-525-674-40	Sequence 40, Appl	779	21	30.9	106	7	US-11-008-727-12	Sequence 12, Appl
707	21.5	31.6	555	7	US-11-034-569-8	Sequence 8, Appli	780	21	30.9	106	7	US-11-073-222-3	Sequence 3, Appli
708	21.5	31.6	560	7	US-11-034-569-6	Sequence 6, Appli	781	21	30.9	106	7	US-11-052-554A-360	Sequence 360, App
709	21.5	31.6	1798	6	US-10-995-561-1033	Sequence 1033, Ap	782	21	30.9	114	6	US-10-986-501-180	Sequence 190, App
710	21.5	31.6	1798	6	US-10-995-561-1034	Sequence 1034, Ap	783	21	30.9	122	6	US-10-467-657-1518	Sequence 1518, Ap
711	21.5	31.6	1886	6	US-10-515-868-8	Sequence 8, Appli	784	21	30.9	125	6	US-10-793-626-2246	Sequence 2246, Ap
712	21.5	31.6	3353	6	US-11-037-243-64	Sequence 64, Appl	785	21	30.9	126	6	US-10-793-626-2272	Sequence 2272, Ap
713	21	30.9	9	6	US-10-467-657-4572	Sequence 4572, Ap	786	21	30.9	126	6	US-10-467-657-2050	Sequence 2050, Ap
714	21	30.9	9	7	US-11-033-039-247	Sequence 247, App	787	21	30.9	126	7	US-11-221-900-11	Sequence 11, Appl
715	21	30.9	11	7	US-11-105-708-9	Sequence 9, Appli	788	21	30.9	127	7	US-11-052-554A-312	Sequence 312, App
716	21	30.9	12	7	US-11-038-980-14	Sequence 14, Appl	789	21	30.9	129	6	US-10-501-039-8	Sequence 8, Appli
717	21	30.9	12	6	US-10-763-286A-37	Sequence 37, Appl	790	21	30.9	129	7	US-11-073-222-2	Sequence 2, Appli
718	21	30.9	12	7	US-11-116-144-85	Sequence 85, Appl	791	21	30.9	130	7	US-11-055-822-650	Sequence 690, App
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720	21	30.9	14	6	US-10-467-657-9100	Sequence 9100, Ap	793	21	30.9	137	7	US-11-022-563-225	Sequence 225, App
721	21	30.9	14	7	US-11-033-039-261	Sequence 261, App	794	21	30.9	138	5	US-09-978-360A-483	Sequence 483, App
722	21	30.9	17	6	US-10-939-890-368	Sequence 368, App	795	21	30.9	138	7	US-11-000-463-446	Sequence 446, App
723	21	30.9	18	7	US-10-763-286A-38	Sequence 38, Appl	796	21	30.9	140	6	US-10-980-388-93	Sequence 93, Appl
724	21	30.9	19	6	US-11-196-919-7	Sequence 7, Appli	797	21	30.9	142	6	US-10-467-657-7870	Sequence 7870, Ap
725	21	30.9	21	6	US-10-939-890-369	Sequence 369, App	798	21	30.9	142	6	US-10-856-751-37	Sequence 37, Appl
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729	21	30.9	22	7	US-11-218-880-19	Sequence 19, Appl	802	21	30.9	151	6	US-10-821-234-1320	Sequence 1320, Ap
730	21	30.9	24	6	US-10-989-226-31	Sequence 31, Appl	803	21	30.9	156	6	US-10-467-657-3808	Sequence 3808, Ap
731	21	30.9	24	7	US-11-066-967-58	Sequence 58, Appl	804	21	30.9	157	6	US-10-467-657-4360	Sequence 4360, Ap
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733	21	30.9	30	7	US-11-156-843-57	Sequence 57, Appl	806	21	30.9	159	6	US-10-467-657-5114	Sequence 5114, Ap
734	21	30.9	30	7	US-11-156-843-70	Sequence 70, Appl	807	21	30.9	160	6	US-10-846-1172A-10	Sequence 10, Appl
735	21	30.9	30	7	US-11-156-843-84	Sequence 84, Appl	808	21	30.9	162	5	US-09-978-360A-585	Sequence 585, App
736	21	30.9	30	7	US-11-156-843-86	Sequence 86, Appl	809	21	30.9	162	7	US-11-033-039-246	Sequence 246, App
737	21	30.9	34	6	US-10-467-657-5458	Sequence 89, Appl	810	21	30.9	164	6	US-10-793-626-2398	Sequence 2398, Ap
738	21	30.9	34	7	US-11-121-301-82	Sequence 82, Appl	811	21	30.9	165	6	US-10-467-657-8784	Sequence 8784, Ap
739	21	30.9	35	7	US-11-174-816-82	Sequence 82, Appl	812	21	30.9	166	7	US-11-094-519A-47	Sequence 47, Appl
740	21	30.9	35	7	US-11-174-816-83	Sequence 83, Appl	813	21	30.9	167	6	US-10-467-657-5306	Sequence 5306, App
741	21	30.9	35	7	US-11-174-816-84	Sequence 84, Appl	814	21	30.9	171	6	US-10-714-887-400	Sequence 400, App
742	21	30.9	35	7	US-11-174-819-101	Sequence 101, App	815	21	30.9	174	6	US-11-055-822-838	Sequence 838, App
743	21	30.9	35	7	US-11-174-819-102	Sequence 102, App	816	21	30.9	175	6	US-10-467-657-7504	Sequence 7504, Ap
744	21	30.9	35	7	US-11-174-819-103	Sequence 103, App	817	21	30.9	176	6	US-10-995-561-821	Sequence 821, App
745	21	30.9	38	7	US-11-027-111-22	Sequence 22, Appl	818	21	30.9	177	6	US-10-714-887-444	Sequence 404, App
746	21	30.9	39	6	US-10-467-657-3574	Sequence 3574, Ap	819	21	30.9	183	6	US-10-467-657-8138	Sequence 8138, Ap
747	21	30.9	40	7	US-11-068-783-77	Sequence 77, Appl	820	21	30.9	183	7	US-11-000-463-286	Sequence 286, App
748	21	30.9	43	6	US-10-467-657-7886	Sequence 7886, Ap	821	21	30.9	184	5	US-09-978-360A-539	Sequence 539, App
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750	21	30.9	46	6	US-10-467-657-7732	Sequence 7732, Ap	823	21	30.9	188	6	US-10-467-657-9970	Sequence 920, App
751	21	30.9	51	6	US-10-467-657-9096	Sequence 9096, Ap	824	21	30.9	191	6	US-10-467-657-2212	Sequence 2212, Ap
752	21	30.9	55	6	US-10-467-657-8693	Sequence 8693, Ap	825	21	30.9	191	6	US-10-467-657-4100	Sequence 4100, Ap
753	21	30.9	58	7	US-11-008-570-104	Sequence 104, App	826	21	30.9	191	6	US-10-467-657-7442	Sequence 7442, Ap
754	21	30.9	60	7	US-11-091-668-6	Sequence 6, Appli	827	21	30.9	191	6	US-10-055-877-42	Sequence 42, Appl
755	21	30.9	63	6	US-10-914-391A-6	Sequence 6, Appli	828	21	30.9	191	6	US-10-519-390-6	Sequence 6, Appli

829	21	30.9	191	6	US-10-519-390-23	Sequence 23, Appl	902	21	30.9	272	6	US-10-467-657-6658	Sequence 6658, Ap
830	21	30.9	191	6	US-10-714-887-56	Sequence 56, Appl	903	21	30.9	272	7	US-11-000-463-217	Sequence 277, App
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832	21	30.9	192	7	US-11-033-365-159	Sequence 159, App	905	21	30.9	280	6	US-10-873-528-49	Sequence 49, Appl
833	21	30.9	192	7	US-11-033-365-197	Sequence 197, App	906	21	30.9	281	6	US-10-467-657-1352	Sequence 1352, Ap
834	21	30.9	192	7	US-11-033-365-198	Sequence 198, App	907	21	30.9	282	6	US-10-878-556A-125	Sequence 125, App
835	21	30.9	192	7	US-11-033-365-200	Sequence 200, App	908	21	30.9	283	6	US-10-632-150-50	Sequence 50, Appl
836	21	30.9	192	7	US-11-187-522-1	Sequence 1, Appl	909	21	30.9	283	7	US-11-073-457-50	Sequence 50, Appl
837	21	30.9	193	6	US-10-467-657-674	Sequence 674, App	910	21	30.9	283	7	US-11-073-460-50	Sequence 50, Appl
838	21	30.9	193	7	US-11-033-365-196	Sequence 196, App	911	21	30.9	284	6	US-10-714-887-128	Sequence 128, App
839	21	30.9	196	7	US-11-033-365-199	Sequence 199, App	912	21	30.9	285	7	US-11-082-389-324	Sequence 324, App
840	21	30.9	198	6	US-10-467-657-5440	Sequence 5440, Ap	913	21	30.9	286	6	US-10-954-468-25	Sequence 25, Appl
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842	21	30.9	202	7	US-11-166-412-128	Sequence 128, App	915	21	30.9	287	6	US-10-954-468-17	Sequence 17, Appl
843	21	30.9	202	7	US-11-166-412-143	Sequence 143, App	916	21	30.9	287	6	US-10-954-468-24	Sequence 24, Appl
844	21	30.9	208	7	US-11-055-822-462	Sequence 462, App	917	21	30.9	287	7	US-11-080-991-66	Sequence 66, Appl
845	21	30.9	208	7	US-11-055-822-704	Sequence 704, App	918	21	30.9	287	7	US-11-054-281-332	Sequence 322, App
846	21	30.9	208	7	US-11-1070-653-52	Sequence 52, Appl	919	21	30.9	288	6	US-10-467-657-82	Sequence 82, Appl
847	21	30.9	209	5	US-09-978-360A-665	Sequence 665, App	920	21	30.9	288	6	US-10-467-657-5918	Sequence 5918, Ap
848	21	30.9	209	7	US-11-055-822-88	Sequence 88, Appl	921	21	30.9	288	6	US-10-954-468-20	Sequence 20, Appl
849	21	30.9	209	7	US-11-055-822-90	Sequence 90, Appl	922	21	30.9	288	6	US-10-954-468-22	Sequence 22, Appl
850	21	30.9	210	5	US-09-978-360A-538	Sequence 538, App	923	21	30.9	288	6	US-10-954-468-23	Sequence 23, Appl
851	21	30.9	211	6	US-10-467-657-6800	Sequence 6800, Ap	924	21	30.9	289	6	US-10-954-468-19	Sequence 19, Appl
852	21	30.9	213	6	US-10-892-379-6	Sequence 6, Appl	925	21	30.9	289	6	US-10-954-468-21	Sequence 21, Appl
853	21	30.9	214	6	US-10-892-379-5	Sequence 5, Appl	926	21	30.9	290	6	US-10-131-826A-222	Sequence 222, App
854	21	30.9	215	6	US-10-996-007B-27	Sequence 27, Appl	927	21	30.9	290	6	US-10-954-468-18	Sequence 18, Appl
855	21	30.9	215	6	US-10-883-512-77	Sequence 77, Appl	928	21	30.9	291	6	US-10-467-657-4148	Sequence 4148, Ap
856	21	30.9	217	6	US-10-467-657-388	Sequence 388, App	929	21	30.9	291	6	US-10-467-657-6508	Sequence 6508, Ap
857	21	30.9	217	6	US-10-467-657-552	Sequence 552, App	930	21	30.9	293	6	US-10-954-468-14	Sequence 14, Appl
858	21	30.9	217	6	US-10-467-657-2380	Sequence 2380, Ap	931	21	30.9	294	6	US-10-467-657-2876	Sequence 2876, Ap
859	21	30.9	217	6	US-10-467-657-3800	Sequence 3800, Ap	932	21	30.9	294	7	US-11-055-822-480	Sequence 480, App
860	21	30.9	217	6	US-10-467-657-3930	Sequence 3930, Ap	933	21	30.9	294	7	US-11-055-822-880	Sequence 880, App
861	21	30.9	217	6	US-10-467-657-4018	Sequence 4018, Ap	934	21	30.9	295	7	US-11-194-246-288	Sequence 288, App
862	21	30.9	217	6	US-10-467-657-4438	Sequence 4438, Ap	935	21	30.9	298	6	US-10-467-657-4362	Sequence 4362, Ap
863	21	30.9	217	6	US-10-467-657-4802	Sequence 4802, Ap	936	21	30.9	298	6	US-10-454-437-384	Sequence 384, App
864	21	30.9	217	6	US-10-467-657-6518	Sequence 6518, Ap	937	21	30.9	298	7	US-11-179-977-6	Sequence 6, Appl
865	21	30.9	217	6	US-10-467-657-8044	Sequence 8044, Ap	938	21	30.9	298	7	US-11-055-822-478	Sequence 478, App
866	21	30.9	218	6	US-10-995-561-830	Sequence 830, App	939	21	30.9	299	6	US-11-055-822-828	Sequence 828, App
867	21	30.9	219	6	US-10-846-172A-1	Sequence 1, Appl	940	21	30.9	299	6	US-10-467-657-4424	Sequence 4424, Ap
868	21	30.9	222	7	US-11-124-368A-208	Sequence 208, App	941	21	30.9	299	6	US-10-878-556A-94	Sequence 94, Appl
869	21	30.9	223	6	US-10-467-657-3574	Sequence 3574, Ap	942	21	30.9	302	6	US-10-467-657-5794	Sequence 5794, Ap
870	21	30.9	224	6	US-10-892-379-7	Sequence 7, Appl	943	21	30.9	303	7	US-11-186-284-193	Sequence 193, App
871	21	30.9	228	6	US-10-467-657-8358	Sequence 8358, Ap	944	21	30.9	303	7	US-11-054-281-82	Sequence 82, Appl
872	21	30.9	232	6	US-10-467-657-4338	Sequence 4338, Ap	945	21	30.9	303	7	US-11-054-281-83	Sequence 83, Appl
873	21	30.9	233	7	US-11-170-653-53	Sequence 53, Appl	946	21	30.9	304	6	US-10-846-172A-5	Sequence 5, Appl
874	21	30.9	234	6	US-10-793-626-2580	Sequence 2580, Ap	947	21	30.9	305	7	US-11-080-991-92	Sequence 92, Appl
875	21	30.9	236	7	US-11-140-965-4	Sequence 4, Appl	948	21	30.9	306	6	US-10-467-657-4304	Sequence 4304, Ap
876	21	30.9	238	7	US-11-008-727-26	Sequence 26, Appl	949	21	30.9	306	7	US-11-102-497-13	Sequence 13, Appl
877	21	30.9	239	7	US-11-000-463-875	Sequence 876, App	950	21	30.9	308	6	US-10-467-657-1236	Sequence 1236, Ap
878	21	30.9	242	7	US-11-150-883-12	Sequence 12, Appl	951	21	30.9	309	6	US-10-524-667-110	Sequence 110, App
879	21	30.9	243	6	US-10-131-826A-164	Sequence 164, App	952	21	30.9	309	6	US-10-714-887-52	Sequence 62, Appl
880	21	30.9	244	6	US-10-793-626-134	Sequence 134, App	953	21	30.9	310	6	US-10-714-887-52	Sequence 52, Appl
881	21	30.9	245	6	US-10-793-626-1042	Sequence 1042, Ap	954	21	30.9	310	7	US-11-082-389-306	Sequence 306, App
882	21	30.9	250	7	US-11-054-515-933	Sequence 933, App	955	21	30.9	311	7	US-11-055-153-7	Sequence 7, Appl
883	21	30.9	253	7	US-11-080-991-42	Sequence 42, Appl	956	21	30.9	311	7	US-11-055-822-246	Sequence 246, App
884	21	30.9	254	6	US-10-467-657-5138	Sequence 5138, Ap	957	21	30.9	312	7	US-11-156-084-202	Sequence 202, App
885	21	30.9	254	7	US-11-067-323-1033	Sequence 1033, Ap	958	21	30.9	312	7	US-11-008-570-41	Sequence 41, Appl
886	21	30.9	254	7	US-11-067-323-1081	Sequence 1081, Ap	959	21	30.9	313	7	US-11-057-554A-316	Sequence 316, App
887	21	30.9	255	6	US-10-846-172A-4	Sequence 4, Appl	960	21	30.9	313	7	US-11-008-570-43	Sequence 43, Appl
888	21	30.9	257	6	US-10-793-626-3344	Sequence 3244, Ap	961	21	30.9	313	7	US-11-152-569-13	Sequence 13, Appl
889	21	30.9	258	7	US-11-054-515-1365	Sequence 1365, Ap	962	21	30.9	313	7	US-11-024-959-356	Sequence 356, App
890	21	30.9	259	6	US-10-467-657-3110	Sequence 3410, Ap	963	21	30.9	313	7	US-11-054-261-18	Sequence 18, Appl
891	21	30.9	259	6	US-10-763-712A-116	Sequence 116, App	964	21	30.9	314	7	US-11-054-281-81	Sequence 81, Appl
892	21	30.9	261	6	US-10-467-657-4282	Sequence 4282, Ap	965	21	30.9	314	7	US-11-183-914-3	Sequence 3, Appl
893	21	30.9	261	6	US-10-613-744-18	Sequence 18, Appl	966	21	30.9	315	6	US-10-467-657-7848	Sequence 7848, Ap
894	21	30.9	262	6	US-10-982-545-3	Sequence 876, App	967	21	30.9	316	7	US-11-055-822-38	Sequence 38, Appl
895	21	30.9	266	6	US-10-821-234-1334	Sequence 1334, Ap	968	21	30.9	317	7	US-10-632-150-42	Sequence 42, Appl
896	21	30.9	266	6	US-10-846-172A-2	Sequence 2, Appl	969	21	30.9	318	6	US-11-073-457-32	Sequence 42, Appl
897	21	30.9	269	6	US-11-000-463-4331	Sequence 403, App	970	21	30.9	318	7	US-11-000-463-331	Sequence 331, App
898	21	30.9	270	7	US-11-008-727-24	Sequence 24, Appl	971	21	30.9	318	7	US-11-000-463-803	Sequence 803, App
899	21	30.9	271	7	US-11-179-977-10	Sequence 10, Appl	972	21	30.9	318	7	US-11-073-460-43	Sequence 42, Appl
900	21	30.9	271	7			973	21	30.9	318	7		
901	21	30.9	271	7			974	21	30.9	318	7		

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975 21 30.9 322 6 US-10-821-234-1092 Sequence 1092, Ap
976 21 30.9 322 6 US-10-878-556A-16 Sequence 16, Appl
977 21 30.9 322 6 US-10-524-647-18 Sequence 18, Appl
978 21 30.9 322 6 US-11-067-121-15 Sequence 15, Appl
979 21 30.9 323 6 US-10-525-674-8 Sequence 8, Appl
980 21 30.9 323 6 US-11-010-239-73 Sequence 73, Appl
981 21 30.9 324 6 US-10-467-657-722 Sequence 722, App
982 21 30.9 326 7 US-11-024-959-446 Sequence 446, App
983 21 30.9 326 7 US-11-024-959-446 Sequence 447, App
984 21 30.9 327 6 US-10-467-962B-107 Sequence 107, App
985 21 30.9 328 6 US-10-995-561-884 Sequence 884, App
986 21 30.9 330 6 US-10-846-172A-7 Sequence 7, Appl
987 21 30.9 331 6 US-11-143-980-57 Sequence 57, Appl
988 21 30.9 332 6 US-10-454-437-28 Sequence 28, Appl
989 21 30.9 332 6 US-10-454-437-42 Sequence 42, Appl
990 21 30.9 333 6 US-10-846-172A-6 Sequence 6, Appl
991 21 30.9 335 6 US-10-995-561-866 Sequence 866, App
992 21 30.9 336 6 US-10-478-345-4 Sequence 4, Appl
993 21 30.9 336 6 US-10-793-626-3210 Sequence 3210, Ap
994 21 30.9 336 7 US-11-152-892-4 Sequence 4, Appl
995 21 30.9 339 6 US-10-821-234-1098 Sequence 1098, Ap
996 21 30.9 340 6 US-10-067-974-8 Sequence 8, Appl
997 21 30.9 340 7 US-11-055-822-42 Sequence 42, Appl
998 21 30.9 342 7 US-11-055-822-452 Sequence 452, App
999 21 30.9 342 7 US-11-152-892-11 Sequence 11, Appl
1000 21 30.9 343 7 US-11-009-658-32 Sequence 32, Appl
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ALIGNMENTS

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RESULT 1
US-11-112-277-16
; Sequence 16, Application US/11112277
; Publication No. US20050267293A1
; GENERAL INFORMATION:
; APPLICANT: Bouquet-Gagnon, Nathalie
; APPLICANT: Quraishi, Omar
; APPLICANT: Bridon, Dominique P.
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN
; FILE REFERENCE: 500862003700
; CURRENT APPLICATION NUMBER: US/11/112,277
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/565,228
; PRIOR FILING DATE: 2004-04-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 28
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ANP Analogue
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa is Ser linked to ABEA-MPA
US-11-112-277-16

Query Match      80.9%; Score 55; DB 7; Length 28;
Best Local Similarity 58.8%; Pred. No. 1.5e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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; GENERAL INFORMATION:
; APPLICANT: Bouquet-Gagnon, Nathalie
; APPLICANT: Quraishi, Omar
; APPLICANT: Bridon, Dominique P.
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN
; FILE REFERENCE: 500862003700
; CURRENT APPLICATION NUMBER: US/11/112,277
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/565,228
; PRIOR FILING DATE: 2004-04-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 28
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ANP Analogue
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa is Ser linked to MPA
US-11-112-277-50

Query Match      80.9%; Score 55; DB 7; Length 28;
Best Local Similarity 58.8%; Pred. No. 1.5e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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OY      1 CFGXXDRIGXXSXXGC 17
      ||| ||| ||| |||
Db      7 CFGGRMDRIGAGSLGC 23
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RESULT 3
US-11-112-277-51
; Sequence 51, Application US/11112277
; Publication No. US20050267293A1
; GENERAL INFORMATION:
; APPLICANT: Bouquet-Gagnon, Nathalie
; APPLICANT: Quraishi, Omar
; APPLICANT: Bridon, Dominique P.
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN
; FILE REFERENCE: 500862003700
; CURRENT APPLICATION NUMBER: US/11/112,277
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/565,228
; PRIOR FILING DATE: 2004-04-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 28
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ANP Analogue
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa is Ser linked to BEEP-MPA
US-11-112-277-51
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Query Match      80.9%; Score 55; DB 7; Length 28;
Best Local Similarity 58.8%; Pred. No. 1.5e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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OY      1 CFGXXDRIGXXSXXGC 17
      ||| ||| ||| |||
Db      7 CFGGRMDRIGAGSLGC 23
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RESULT 4
US-11-112-277-50
; Sequence 50, Application US/11112277
; Publication No. US20050267293A1
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US-11-059-814-4
; Sequence 4, Application US/11059814
; Publication No. US20050272650A1
; GENERAL INFORMATION:
; APPLICANT: University of South Florida
; APPLICANT: Mohapatra, Shyam
; TITLE OF INVENTION: Materials and Methods for Treatment of Inflammatory and Cell
; FILE REFERENCE: USF-215PTC2
; CURRENT APPLICATION NUMBER: US/11/059,814
; PRIOR FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: 60/521,072
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-059-814-4

Query Match 80.9%; Score 55; DB 7; Length 28;
Best Local Similarity 58.8%; Pred. No. 1.5e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXXGC 17
DB 7 CFGGRMDRIGAGSGGCG 23

RESULT 5
US-11-175-690-309
; Sequence 309, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haselkline et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 309
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-309

Query Match 80.9%; Score 55; DB 7; Length 28;
Best Local Similarity 58.8%; Pred. No. 1.5e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXXGC 17
DB 7 CFGGRMDRIGAGSGGCG 23

RESULT 6
US-10-510-880-3
; Sequence 3, Application US/10510880
; Publication No. US20050244902A1
; GENERAL INFORMATION:
; APPLICANT: Rehfeld, Jens F.
; APPLICANT: Goetze, Jens Peter
; APPLICANT: Righspospitalet
; TITLE OF INVENTION: Methods for determining levels of human
; FILE REFERENCE: 271212000200
; CURRENT APPLICATION NUMBER: US/10/510,880
; PRIOR FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: PCT/DK03/00250
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: PSI692
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-510-880-3

Query Match 80.9%; Score 55; DB 6; Length 121;
Best Local Similarity 58.8%; Pred. No. 5.9e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXXGC 17
DB 99 CFGHKIDRIGSVRLGC 115

RESULT 7
US-10-977-334-5
; Sequence 5, Application US/10977334
; Publication No. US20050244904A1
; GENERAL INFORMATION:
; APPLICANT: NG, LEONG
; TITLE OF INVENTION: DIAGNOSTICS BASED ON SIGNAL PEPTIDE DETECTION
; FILE REFERENCE: ISA-016.01
; CURRENT APPLICATION NUMBER: US/10/977,334
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: 60/542,647
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: GB 0325279.8
; PRIOR FILING DATE: 2003-10-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 5
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-977-334-5

Query Match 80.9%; Score 55; DB 6; Length 126;
Best Local Similarity 58.8%; Pred. No. 6.1e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXDRIGXXSXXGC 17
DB 110 CFGKLDRIGSMGCG 126

RESULT 8
US-10-510-880-2
; Sequence 2, Application US/10510880
; Publication No. US20050244902A1
; GENERAL INFORMATION:
; APPLICANT: Rehfeld, Jens F.
; APPLICANT: Goetze, Jens Peter
; APPLICANT: Righspospitalet

```

; TITLE OF INVENTION: Methods for determining levels of human
; FILE REFERENCE: 271212000200
; CURRENT APPLICATION NUMBER: US/10/510,880
; PRIOR FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: PCT/DK03/00250
; PRIOR FILING DATE: 2003-04-11
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 131
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-510-880-2

Query Match      80.9%; Score 55; DB 6; Length 131;
Best Local Similarity 58.8%; Pred. No. 6.3e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      1 CFGXXXDRIGXXSXXGC 17
      ||| ||| | ||
Db      109 CFGRRUDRIGSLGSLGCG 125

RESULT 9
US-11-059-814-7
; Sequence 7, Application US/11059814
; Publication No. US20050272650A1
; GENERAL INFORMATION:
; APPLICANT: University of South Florida
; APPLICANT: Mohapatra, Shyam
; TITLE OF INVENTION: Materials and Methods for Treatment of Inflammatory and Cell
; FILE REFERENCE: USF-215PTCZ
; CURRENT APPLICATION NUMBER: US/11/059,814
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: 60/521,072
; PRIOR FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 7
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-059-814-7

Query Match      80.9%; Score 55; DB 7; Length 151;
Best Local Similarity 58.8%; Pred. No. 7.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      1 CFGXXXDRIGXXSXXGC 17
      ||| ||| | ||
Db      130 CFGGRMDRIGAGSLGCG 146

RESULT 10
US-11-059-814-16
; Sequence 16, Application US/11059814
; Publication No. US20050272650A1
; GENERAL INFORMATION:
; APPLICANT: University of South Florida
; APPLICANT: Mohapatra, Shyam
; TITLE OF INVENTION: Materials and Methods for Treatment of Inflammatory and Cell
; FILE REFERENCE: USF-215PTCZ
; CURRENT APPLICATION NUMBER: US/11/059,814
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: 60/521,072
; PRIOR FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
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; SEQ ID NO: 15
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-059-814-16

Query Match      80.9%; Score 55; DB 7; Length 152;
Best Local Similarity 58.8%; Pred. No. 7.3e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      1 CFGXXXDRIGXXSXXGC 17
      ||| ||| | ||
Db      129 CFGGRIDRIGAGSLGCG 145

RESULT 11
US-10-977-334-4
; Sequence 4, Application US/10977334
; Publication No. US20050244904A1
; GENERAL INFORMATION:
; APPLICANT: NG, LEONG
; TITLE OF INVENTION: DIAGNOSTICS BASED ON SIGNAL PEPTIDE DETECTION
; FILE REFERENCE: ISA-016.01
; CURRENT APPLICATION NUMBER: US/10/977,334
; CURRENT FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: 60/542,647
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: GB 0325279.8
; PRIOR FILING DATE: 2003-10-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO: 4
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-977-334-4

Query Match      80.9%; Score 55; DB 6; Length 153;
Best Local Similarity 58.8%; Pred. No. 7.3e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      1 CFGXXXDRIGXXSXXGC 17
      ||| ||| | ||
Db      130 CFGGRMDRIGAGSLGCG 146

RESULT 12
US-11-175-690-222
; Sequence 222, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 222
LENGTH: 637
TYPE: PRT
ORGANISM: Homo sapiens
US-11-175-690-222

Query Match
Best Local Similarity 80.9%; Score 55; DB 7; Length 637;
Best Local Similarity 58.8%; Pred. No. 0.00027;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXXXC 17
Db 31 CFGGRMDRIGAQSGLCG 47

RESULT 13
US-11-175-690-321
Sequence 321, Application US/11175690
Publication No. US20060014254A1

GENERAL INFORMATION:
APPLICANT: Haseltine et al.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF605
CURRENT APPLICATION NUMBER: US/11/175,690
CURRENT FILING DATE: 2005-07-07
PRIOR APPLICATION NUMBER: PCT/US04/001369
PRIOR FILING DATE: 2004-01-20
PRIOR APPLICATION NUMBER: US 60/441,305
PRIOR FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: US 60/453,201
PRIOR FILING DATE: 2003-03-11
PRIOR APPLICATION NUMBER: US 60/467,222
PRIOR FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: US 60/472,816
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 60/476,267
PRIOR FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: US 60/505,172
PRIOR FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: US 60/506,746
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 568
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 321
LENGTH: 26
TYPE: PRT
ORGANISM: Homo sapiens
US-11-175-690-321

Query Match
Best Local Similarity 73.5%; Score 50; DB 7; Length 26;
Best Local Similarity 52.9%; Pred. No. 0.00016;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXXXC 17
Db 10 CFGGRMDRISSSSGLCG 26

RESULT 14
US-11-175-690-322
Sequence 322, Application US/11175690
Publication No. US20060014254A1

GENERAL INFORMATION:
APPLICANT: Haseltine et al.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF605
CURRENT APPLICATION NUMBER: US/11/175,690
CURRENT FILING DATE: 2005-07-07
PRIOR APPLICATION NUMBER: PCT/US04/001369
PRIOR FILING DATE: 2004-01-20
PRIOR APPLICATION NUMBER: US 60/441,305
PRIOR FILING DATE: 2003-01-22

PRIOR APPLICATION NUMBER: US 60/453,201
PRIOR FILING DATE: 2003-03-11
PRIOR APPLICATION NUMBER: US 60/467,222
PRIOR FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: US 60/472,816
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 60/476,267
PRIOR FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: US 60/505,172
PRIOR FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: US 60/506,746
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 568
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 322
LENGTH: 27
TYPE: PRT
ORGANISM: Homo sapiens
US-11-175-690-322

Query Match
Best Local Similarity 73.5%; Score 50; DB 7; Length 27;
Best Local Similarity 52.9%; Pred. No. 0.00016;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXXXC 17
Db 10 CFGGRMDRISSSSGLCG 26

RESULT 15
US-11-175-690-371
Sequence 371, Application US/11175690
Publication No. US20060014254A1

GENERAL INFORMATION:
APPLICANT: Haseltine et al.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF605
CURRENT APPLICATION NUMBER: US/11/175,690
CURRENT FILING DATE: 2005-07-07
PRIOR APPLICATION NUMBER: PCT/US04/001369
PRIOR FILING DATE: 2004-01-20
PRIOR APPLICATION NUMBER: US 60/441,305
PRIOR FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: US 60/453,201
PRIOR FILING DATE: 2003-03-11
PRIOR APPLICATION NUMBER: US 60/467,222
PRIOR FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: US 60/472,816
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: US 60/476,267
PRIOR FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: US 60/505,172
PRIOR FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: US 60/506,746
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 568
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 371
LENGTH: 27
TYPE: PRT
ORGANISM: Homo sapiens
US-11-175-690-371

Query Match
Best Local Similarity 73.5%; Score 50; DB 7; Length 27;
Best Local Similarity 52.9%; Pred. No. 0.00016;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXXXC 17
Db 10 CFGGRMDRISSSSGLCG 26

RESULT 16

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US-11-175-690-323
; Sequence 323, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 323
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-323
```

```
Query Match          73.5%; Score 50; DB 7; Length 28;
Best Local Similarity 52.9%; Pred. No. 0.00017;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
QY      1 CFCGXXDRIGXXSXGC 17
          ||| ||| ||| |||
Db       10 CFCGRMDRISSSSGIGC 26
```

```
RESULT 17
; Sequence 369, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 369
; LENGTH: 28
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-11-175-690-369
```

```
Query Match          73.5%; Score 50; DB 7; Length 28;
Best Local Similarity 52.9%; Pred. No. 0.00017;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
QY      1 CFCGXXDRIGXXSXGC 17
          ||| ||| ||| |||
Db       10 CFCGRMDRISSSSGIGC 26
```

```
RESULT 18
; Sequence 314, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 314
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-314
```

```
Query Match          73.5%; Score 50; DB 7; Length 29;
Best Local Similarity 52.9%; Pred. No. 0.00018;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
QY      1 CFCGXXDRIGXXSXGC 17
          ||| ||| ||| |||
Db       10 CFCGRMDRISSSSGIGC 26
```

```
RESULT 19
; Sequence 315, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
```


;; PRIOR APPLICATION NUMBER: US 60/472,816
;; PRIOR FILING DATE: 2003-05-23
;; PRIOR APPLICATION NUMBER: US 60/476,267
;; PRIOR FILING DATE: 2003-06-06
;; PRIOR APPLICATION NUMBER: US 60/505,172
;; PRIOR FILING DATE: 2003-09-24
;; PRIOR APPLICATION NUMBER: US 60/506,746
;; PRIOR FILING DATE: 2003-09-30
;; NUMBER OF SEQ ID NOS: 568
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 315
;; LENGTH: 29
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-175-690-315

Query Match 73.5%; Score 50; DB 7; Length 29;
Best Local Similarity 52.9%; Pred. No. 0.00018;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 CFCGXXDRIGXXSXGC 17
DB 10 CFCGKMDRISSSSGIGC 26

RESULT 20
US-10-510-880-4
;; Sequence 4, Application US/10510880
;; Publication No. US20050244902A1
;; GENERAL INFORMATION:
;; APPLICANT: Goetze, Jens F.
;; APPLICANT: Rehfeld, Jens Peter
;; APPLICANT: Righospitale
;; TITLE OF INVENTION: Methods for determining levels of human
;; FILE REFERENCE: 271212000200
;; CURRENT APPLICATION NUMBER: US/10/510,880
;; CURRENT FILING DATE: 2004-10-08
;; PRIOR APPLICATION NUMBER: PCT/DK03/00250
;; PRIOR FILING DATE: 2003-04-11
;; PRIOR APPLICATION NUMBER: PS1692
;; PRIOR FILING DATE: 2002-04-11
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 4
;; LENGTH: 32
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-510-880-4

Query Match 73.5%; Score 50; DB 6; Length 32;
Best Local Similarity 52.9%; Pred. No. 0.00019;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 CFCGXXDRIGXXSXGC 17
DB 10 CFCGKMDRISSSSGIGC 26

RESULT 21
US-10-977-334-3
;; Sequence 3, Application US/10977334
;; Publication No. US20050244904A1
;; GENERAL INFORMATION:
;; APPLICANT: NG, LEONG
;; TITLE OF INVENTION: DIAGNOSTICS BASED ON SIGNAL PEPTIDE DETECTION
;; FILE REFERENCE: ISA-016.01
;; CURRENT APPLICATION NUMBER: US/10/977,334
;; CURRENT FILING DATE: 2004-10-29
;; PRIOR APPLICATION NUMBER: 60/542,647
;; PRIOR FILING DATE: 2004-02-06
;; PRIOR APPLICATION NUMBER: GB 0325279.8
;; PRIOR FILING DATE: 2003-10-29

;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: PatentIn Ver. 3.3
;; SEQ ID NO 3
;; LENGTH: 32
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-977-334-3

Query Match 73.5%; Score 50; DB 6; Length 32;
Best Local Similarity 52.9%; Pred. No. 0.00019;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 CFCGXXDRIGXXSXGC 17
DB 10 CFCGKMDRISSSSGIGC 26

RESULT 22
US-11-043-590-17
;; Sequence 17, Application US/11043590
;; Publication No. US20050277156A1
;; GENERAL INFORMATION:
;; APPLICANT: Compugen Ltd
;; TITLE OF INVENTION: Novel Brain Natriuretic Peptide Variants and Methods of use the
;; FILE REFERENCE: 1847.1011
;; CURRENT APPLICATION NUMBER: US/11/043,590
;; CURRENT FILING DATE: 2005-01-27
;; NUMBER OF SEQ ID NOS: 47
;; SEQ ID NO 17
;; LENGTH: 32
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-043-590-17

Query Match 73.5%; Score 50; DB 7; Length 32;
Best Local Similarity 52.9%; Pred. No. 0.00019;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 CFCGXXDRIGXXSXGC 17
DB 10 CFCGKMDRISSSSGIGC 26

RESULT 23
US-11-175-690-288
;; Sequence 288, Application US/11175690
;; Publication No. US20060014254A1
;; GENERAL INFORMATION:
;; APPLICANT: Haseltine et al.
;; TITLE OF INVENTION: Albumin Fusion Proteins
;; FILE REFERENCE: PF605
;; CURRENT APPLICATION NUMBER: US/11/175,690
;; CURRENT FILING DATE: 2005-07-07
;; PRIOR APPLICATION NUMBER: PCT/US04/001369
;; PRIOR FILING DATE: 2004-01-20
;; PRIOR APPLICATION NUMBER: US 60/441,305
;; PRIOR FILING DATE: 2003-01-22
;; PRIOR APPLICATION NUMBER: US 60/453,201
;; PRIOR FILING DATE: 2003-03-11
;; PRIOR APPLICATION NUMBER: US 60/467,222
;; PRIOR FILING DATE: 2003-05-02
;; PRIOR APPLICATION NUMBER: US 60/472,816
;; PRIOR FILING DATE: 2003-05-23
;; PRIOR APPLICATION NUMBER: US 60/476,267
;; PRIOR FILING DATE: 2003-06-06
;; PRIOR APPLICATION NUMBER: US 60/505,172
;; PRIOR FILING DATE: 2003-09-24
;; PRIOR APPLICATION NUMBER: US 60/506,746
;; PRIOR FILING DATE: 2003-09-30
;; NUMBER OF SEQ ID NOS: 568
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 288
;; LENGTH: 32

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-288

Query Match
  73.5%; Score 50; DB 7; Length 32;
  Best Local Similarity 52.9%; Pred. No. 0.00019;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
   ||| ||| |||
Db 10 CFGRKMDRISSSSGIGGC 26

RESULT 24
US-11-175-690-298
; Sequence 298, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 298
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-298

Query Match
  73.5%; Score 50; DB 7; Length 32;
  Best Local Similarity 52.9%; Pred. No. 0.00019;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
   ||| ||| |||
Db 10 CFGRKMDRISSSSGIGGC 26

RESULT 25
US-11-175-690-304
; Sequence 304, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
```

```
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 304
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-304

Query Match
  73.5%; Score 50; DB 7; Length 32;
  Best Local Similarity 52.9%; Pred. No. 0.00019;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
   ||| ||| |||
Db 10 CFGRKMDRISSSSGIGGC 26

RESULT 26
US-11-175-690-317
; Sequence 317, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 317
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-317

Query Match
  73.5%; Score 50; DB 7; Length 32;
  Best Local Similarity 52.9%; Pred. No. 0.00019;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
   ||| ||| |||
Db 10 CFGRKMDRISSSSGIGGC 26

RESULT 27
US-11-175-690-318
; Sequence 318, Application US/11175690
; Publication No. US20060014254A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Haselaine et al.
/ TITLE OF INVENTION: Albumin Fusion Proteins
/ FILE REFERENCE: PF605
/ CURRENT APPLICATION NUMBER: US/11/175,690
/ PRIOR FILING DATE: 2005-07-07
/ PRIOR APPLICATION NUMBER: PCT/US04/001369
/ PRIOR FILING DATE: 2004-01-20
/ PRIOR APPLICATION NUMBER: US 60/441,305
/ PRIOR FILING DATE: 2003-01-22
/ PRIOR APPLICATION NUMBER: US 60/453,201
/ PRIOR FILING DATE: 2003-03-11
/ PRIOR APPLICATION NUMBER: US 60/467,222
/ PRIOR FILING DATE: 2003-05-02
/ PRIOR APPLICATION NUMBER: US 60/472,816
/ PRIOR FILING DATE: 2003-05-23
/ PRIOR APPLICATION NUMBER: US 60/476,267
/ PRIOR FILING DATE: 2003-06-06
/ PRIOR APPLICATION NUMBER: US 60/505,172
/ PRIOR FILING DATE: 2003-09-24
/ PRIOR APPLICATION NUMBER: US 60/506,746
/ NUMBER OF SEQ ID NOS: 568
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 370
/ LENGTH: 32
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-175-690-318

Query Match      73.5%; Score 50; DB 7; Length 32;
Best Local Similarity 52.9%; Pred. No. 0.00019;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
Qy      1 CCGXXXDRIGXXXGXC 17
Db      10 CCGRMKMDRISSSSGLGC 26
```

```
RESULT 28
US-11-175-690-370
/ Sequence 370, Application US/11/175690
/ Publication No. US20060014254A1
/ GENERAL INFORMATION:
/ APPLICANT: Haselaine et al.
/ TITLE OF INVENTION: Albumin Fusion Proteins
/ FILE REFERENCE: PF605
/ CURRENT APPLICATION NUMBER: US/11/175,690
/ PRIOR FILING DATE: 2005-07-07
/ PRIOR APPLICATION NUMBER: PCT/US04/001369
/ PRIOR FILING DATE: 2004-01-20
/ PRIOR APPLICATION NUMBER: US 60/441,305
/ PRIOR FILING DATE: 2003-01-22
/ PRIOR APPLICATION NUMBER: US 60/453,201
/ PRIOR FILING DATE: 2003-03-11
/ PRIOR APPLICATION NUMBER: US 60/467,222
/ PRIOR FILING DATE: 2003-05-02
/ PRIOR APPLICATION NUMBER: US 60/472,816
/ PRIOR FILING DATE: 2003-05-23
/ PRIOR APPLICATION NUMBER: US 60/476,267
/ PRIOR FILING DATE: 2003-06-06
/ PRIOR APPLICATION NUMBER: US 60/505,172
/ PRIOR FILING DATE: 2003-09-24
/ PRIOR APPLICATION NUMBER: US 60/506,746
/ NUMBER OF SEQ ID NOS: 568
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 370
/ LENGTH: 32
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-175-690-370
```

```
Query Match      73.5%; Score 50; DB 7; Length 32;
Best Local Similarity 52.9%; Pred. No. 0.00019;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
Qy      1 CCGXXXDRIGXXXGXC 17
Db      10 CCGRMKMDRISSSSGLGC 26
```

```
RESULT 29
US-11-043-590-15
/ Sequence 15, Application US/11043590
/ Publication No. US20050277156A1
/ GENERAL INFORMATION:
/ APPLICANT: Compugen Ltd
/ TITLE OF INVENTION: Novel Brain Natriuretic Peptide Variants and Methods of use therefor
/ FILE REFERENCE: 1847.1011
/ CURRENT APPLICATION NUMBER: US/11/043,590
/ PRIOR FILING DATE: 2005-01-27
/ NUMBER OF SEQ ID NOS: 47
/ SEQ ID NO 15
/ LENGTH: 42
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-043-590-15
```

```
Query Match      73.5%; Score 50; DB 7; Length 42;
Best Local Similarity 52.9%; Pred. No. 0.00025;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
Qy      1 CCGXXXDRIGXXXGXC 17
Db      20 CCGRMKMDRISSSSGLGC 36
```

```
RESULT 30
US-11-175-690-368
/ Sequence 368, Application US/11/175690
/ Publication No. US20060014254A1
/ GENERAL INFORMATION:
/ APPLICANT: Haselaine et al.
/ TITLE OF INVENTION: Albumin Fusion Proteins
/ FILE REFERENCE: PF605
/ CURRENT APPLICATION NUMBER: US/11/175,690
/ PRIOR FILING DATE: 2005-07-07
/ PRIOR APPLICATION NUMBER: PCT/US04/001369
/ PRIOR FILING DATE: 2004-01-20
/ PRIOR APPLICATION NUMBER: US 60/441,305
/ PRIOR FILING DATE: 2003-01-22
/ PRIOR APPLICATION NUMBER: US 60/453,201
/ PRIOR FILING DATE: 2003-03-11
/ PRIOR APPLICATION NUMBER: US 60/467,222
/ PRIOR FILING DATE: 2003-05-02
/ PRIOR APPLICATION NUMBER: US 60/472,816
/ PRIOR FILING DATE: 2003-05-23
/ PRIOR APPLICATION NUMBER: US 60/476,267
/ PRIOR FILING DATE: 2003-06-06
/ PRIOR APPLICATION NUMBER: US 60/505,172
/ PRIOR FILING DATE: 2003-09-24
/ PRIOR APPLICATION NUMBER: US 60/506,746
/ NUMBER OF SEQ ID NOS: 568
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 368
/ LENGTH: 52
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-175-690-368
```

```
Query Match      73.5%; Score 50; DB 7; Length 52;
Best Local Similarity 52.9%; Pred. No. 0.0003;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
QY      1  CCGXXXXRIGXXSXXGC 17
      ||| ||| ||| |||
Db      10  CCGRKMMDRISSSSGLGC 26

RESULT 31
US-11-043-590-16
; Sequence 16, Application US/11043590
; Publication No. US20050277156A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: Novel Brain Natriuretic Peptide Variants and Methods of use there
; FILE REFERENCE: 1847.1011
; CURRENT APPLICATION NUMBER: US/11/043,590
; PRIOR FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 16
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-590-16

Query Match      73.5%; Score 50; DB 7; Length 60;
Best Local Similarity 52.9%; Pred. No. 0.00034;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1  CCGXXXXRIGXXSXXGC 17
      ||| ||| ||| |||
Db      10  CCGRKMMDRISSSSGLGC 26

RESULT 32
US-10-510-880-5
; Sequence 5, Application US/10510880
; Publication No. US20050244902A1
; GENERAL INFORMATION:
; APPLICANT: Rehfeld, Jens F.
; APPLICANT: Goetze, Jens Peter
; APPLICANT: Righospitale
; TITLE OF INVENTION: Methode for determining levels of human
; FILE REFERENCE: 271212000200
; CURRENT APPLICATION NUMBER: US/10/510,880
; PRIOR FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: PCT/DK03/00250
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: PS1692
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-510-880-5

Query Match      73.5%; Score 50; DB 6; Length 108;
Best Local Similarity 52.9%; Pred. No. 0.00059;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1  CCGXXXXRIGXXSXXGC 17
      ||| ||| ||| |||
Db      86  CCGRKMMDRISSSSGLGC 102

RESULT 33
US-10-875-800-1
; Sequence 1, Application US/10875800
; Publication No. US20050255484A1
; GENERAL INFORMATION:
; APPLICANT: VALKIRS, GUNARS
; APPLICANT: DAHLEN, JEFF
; APPLICANT: KIRCHICK, HOWARD
```

```
; APPLICANT: BUECHLER, KEN
; TITLE OF INVENTION: DIAGNOSTIC MARKERS OF STROKE AND CEREBRAL INJURY AND
; FILE REFERENCE: 071949-5408
; CURRENT APPLICATION NUMBER: US/10/875,800
; PRIOR FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/10/714,078
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 10/371,149
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 10/225,082
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT/US02/26604
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/313,775
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/334,964
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/346,485
; PRIOR FILING DATE: 2002-01-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-875-800-1

Query Match      73.5%; Score 50; DB 6; Length 108;
Best Local Similarity 52.9%; Pred. No. 0.00059;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1  CCGXXXXRIGXXSXXGC 17
      ||| ||| ||| |||
Db      86  CCGRKMMDRISSSSGLGC 102

RESULT 34
US-10-299-977-1
; Sequence 1, Application US/10299977
; Publication No. US20050287613A1
; GENERAL INFORMATION:
; APPLICANT: Kupchak, Peter
; APPLICANT: Stanton, Eric
; APPLICANT: Davey, Michelle
; TITLE OF INVENTION: Polyclonal-Polyclonal ELISA Assay for Detecting N-Terminus ProBNP
; FILE REFERENCE: 2132.127
; CURRENT APPLICATION NUMBER: US/10/299,977
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-299-977-1

Query Match      73.5%; Score 50; DB 6; Length 108;
Best Local Similarity 52.9%; Pred. No. 0.00059;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1  CCGXXXXRIGXXSXXGC 17
      ||| ||| ||| |||
Db      86  CCGRKMMDRISSSSGLGC 102

RESULT 35
US-10-510-880-1
; Sequence 1, Application US/10510880
; Publication No. US20050244902A1
; GENERAL INFORMATION:
; APPLICANT: Rehfeld, Jens F.
```

```

; APPLICANT: Goetze, Jens Peter
; APPLICANT: Rhipospitaler
; TITLE OF INVENTION: Methode for determining levels of human
; FILE REFERENCE: 271212000200
; CURRENT APPLICATION NUMBER: US/10/510,880
; PRIOR FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: PCT/DK03/00250
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: PS1692
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-510-880-1

```

Query Match 73.5%; Score 50; DB 6; Length 134;
 Best Local Similarity 52.9%; Pred. No. 0.00072;
 Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

Qy 1 CFGXXXDRIGXXSXXGC 17
Db 112 CFGRKMDRISSSSGLGC 128

```

```

RESULT 36
US-10-875-800-2
; Sequence 2, Application US/10875800
; Publication No. US20050255484A1
; GENERAL INFORMATION:
; APPLICANT: VALKIRS, GUNARS
; APPLICANT: DAHLEN, JEFF
; APPLICANT: KIRCHICK, HOWARD
; APPLICANT: BUECHLER, KEN
; TITLE OF INVENTION: DIAGNOSTIC MARKERS OF STROKE AND CEREBRAL INJURY AND
; FILE REFERENCE: 071949-5408
; CURRENT APPLICATION NUMBER: US/10/875,800
; PRIOR FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/10/714,078
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 10/371,149
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 10/225,082
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT/US02/26604
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/313,775
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/334,964
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/346,485
; PRIOR FILING DATE: 2002-01-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-875-800-2

```

Query Match 73.5%; Score 50; DB 6; Length 134;
 Best Local Similarity 52.9%; Pred. No. 0.00072;
 Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

Qy 1 CFGXXXDRIGXXSXXGC 17
Db 112 CFGRKMDRISSSSGLGC 128

```

```

RESULT 37
US-11-043-590-12
; Sequence 12, Application US/11043590
; Publication No. US20050277156A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: Novel Brain Natriuretic Peptide Variants and Methods of use the
; FILE REFERENCE: 1847.1011
; CURRENT APPLICATION NUMBER: US/11/043,590
; PRIOR FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 12
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-590-12

```

Query Match 73.5%; Score 50; DB 7; Length 134;
 Best Local Similarity 52.9%; Pred. No. 0.00072;
 Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

Qy 1 CFGXXXDRIGXXSXXGC 17
Db 112 CFGRKMDRISSSSGLGC 128

```

```

RESULT 38
US-11-043-590-13
; Sequence 13, Application US/11043590
; Publication No. US20050277156A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: Novel Brain Natriuretic Peptide Variants and Methods of use the
; FILE REFERENCE: 1847.1011
; CURRENT APPLICATION NUMBER: US/11/043,590
; PRIOR FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 13
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-590-13

```

Query Match 73.5%; Score 50; DB 7; Length 162;
 Best Local Similarity 52.9%; Pred. No. 0.00086;
 Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

Qy 1 CFGXXXDRIGXXSXXGC 17
Db 112 CFGRKMDRISSSSGLGC 128

```

```

RESULT 39
US-11-175-690-234
; Sequence 234, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; PRIOR FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267

```

```

; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 234
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-234

Query Match      73.5%; Score 50; DB 7; Length 630;
Best Local Similarity 52.9%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CPGXXXDRIGXXXGXC 17
      ||| ||| ||| |||
Db      29 CPGKMDRISSSGLGCC 45

RESULT 40
US-11-175-690-235
; Sequence 235, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 235
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-235

Query Match      73.5%; Score 50; DB 7; Length 631;
Best Local Similarity 52.9%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CPGXXXDRIGXXXGXC 17
      ||| ||| ||| |||
Db      29 CPGKMDRISSSGLGCC 45

RESULT 41
US-11-175-690-236
; Sequence 236, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
```

```

; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 236
; LENGTH: 632
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-236

Query Match      73.5%; Score 50; DB 7; Length 632;
Best Local Similarity 52.9%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CPGXXXDRIGXXXGXC 17
      ||| ||| ||| |||
Db      29 CPGKMDRISSSGLGCC 45
```

```

RESULT 42
US-11-175-690-228
; Sequence 228, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 228
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-228

Query Match      73.5%; Score 50; DB 7; Length 633;
Best Local Similarity 52.9%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

Oy 1 CFCGXXDRIGXXSXXGC 17
||| ||| |||
Db 29 CFCGKMDRISSSSGIGC 45

RESULT 43

US-11-175-690-211
; Sequence 211, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-211

Query Match 73.5%; Score 50; DB 7; Length 641;
Best Local Similarity 52.9%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 1 CFCGXXDRIGXXSXXGC 17
||| ||| |||
Db 34 CFCGKMDRISSSSGIGC 50

RESULT 44

US-11-175-690-230
; Sequence 230, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746

; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 230
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-230

Query Match 73.5%; Score 50; DB 7; Length 641;
Best Local Similarity 52.9%; Pred. No. 0.003;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 1 CFCGXXDRIGXXSXXGC 17
||| ||| |||
Db 34 CFCGKMDRISSSSGIGC 50

RESULT 45

US-11-175-690-281
; Sequence 281, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 281
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-281

Query Match 73.5%; Score 50; DB 7; Length 661;
Best Local Similarity 52.9%; Pred. No. 0.0031;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 1 CFCGXXDRIGXXSXXGC 17
||| ||| |||
Db 34 CFCGKMDRISSSSGIGC 50

RESULT 46

US-11-175-690-284
; Sequence 284, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20

```
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 284
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-284
```

```
Query Match          73.5%; Score 50; DB 7; Length 663;
Best Local Similarity 52.9%; Pred. No. 0.0031;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
Qy      1 CFCGXXDRIGXXSXXGC 17
      ||| ||| ||| |||
Db      34 CFCGRKMDRISSSSGGLGC 50
```

```
RESULT 47
US-11-175-690-282
; Sequence 282, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 282
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-282
```

```
Query Match          73.5%; Score 50; DB 7; Length 665;
Best Local Similarity 52.9%; Pred. No. 0.0031;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
Qy      1 CFCGXXDRIGXXSXXGC 17
      ||| ||| ||| |||
Db      34 CFCGRKMDRISSSSGGLGC 50
```

```
RESULT 48
US-11-175-690-227
; Sequence 227, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 283
```

```
Query Match          73.5%; Score 50; DB 7; Length 667;
Best Local Similarity 52.9%; Pred. No. 0.0032;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
Qy      1 CFCGXXDRIGXXSXXGC 17
      ||| ||| ||| |||
Db      34 CFCGRKMDRISSSSGGLGC 50
```

```
RESULT 49
US-11-175-690-283
; Sequence 283, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 283
```


Fri Jan 27 10:40:56 2006

LENGTH: 670
TYPE: PRT
ORGANISM: Homo sapiens
US-11-175-690-283

Query Match 73.5%; Score 50; DB 7; Length 670;
Best Local Similarity 52.9%; Pred. No. 0.0032;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CPGXXXDRIGXXXGCC 17
Db 31 CPGRKMDRISSSSGLCG 47

RESULT 50
US-11-175-690-201

; Sequence 201, Application US/1175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
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; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 201
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-175-690-201

Query Match 73.5%; Score 50; DB 7; Length 673;
Best Local Similarity 52.9%; Pred. No. 0.0032;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CPGXXXDRIGXXXGCC 17
Db 34 CPGRKMDRISSSSGLCG 50

Search completed: January 26, 2006, 14:47:30
Job time : 9 secs

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OM protein - protein search, using sw model

Run on: January 26, 2006, 14:38:26 : Search time 77 Seconds
(without alignments)
97.006 Million cell updates/sec

Title: US-10-664-605-5

Perfect score: 68

Sequence: 1 CFGXXDXRIGXKXGC 17

Scoring table:

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Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

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Database :

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1: geneeqp1980s:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	56	82.4	17	5	ABG98241 Human C-T
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5	56	82.4	17	5	ABG98269 Human C-T
6	56	82.4	17	5	ABG98211 Human C-T
7	56	82.4	18	2	ABG98230 Human C-T
8	56	82.4	18	2	ABG98254 Human C-T
9	56	82.4	18	2	ABG98227 Human C-T
10	56	82.4	18	2	ABG98261 Human C-T
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98	55	80.9	18	2	AAR40653	Aar40653 [D-Arg129	171	55	80.9	22	2	AAR36959	Aar36959 ANVP #23.
99	55	80.9	18	2	AAR40605	Aar40605 [Arg129]h	172	55	80.9	22	2	AAR21992	Aar21992 Porcine C
100	55	80.9	18	2	AAR40611	Aar40611 [Arg129]h	173	55	80.9	22	2	AAR70089	Aar70089 Alpha hum
101	55	80.9	18	2	AAR40595	Aar40595 [Arg129]h	174	55	80.9	22	3	AAB24081	AAB24081 Human PRO
102	55	80.9	19	1	AAP80902	Human car	175	55	80.9	22	3	AAB10487	AAB10487 Human C-P
103	55	80.9	20	2	AAR04085	Aar04085 Sequence	176	55	80.9	22	4	AAB82551	AAB82551 Human C-P
104	55	80.9	20	2	AAR40474	Aar40474 [D-Cys145	177	55	80.9	22	4	AAB91332	AAB91332 Brain nat
105	55	80.9	20	2	AAR40397	Aar40397 hANVP (127	178	55	80.9	22	4	AAB91342	AAB91342 C-type na
106	55	80.9	20	2	AAR40403	Aar40403 [D-Cys129	179	55	80.9	22	4	AAB91341	AAB91341 C-type na
107	55	80.9	20	2	AAR40506	Aar40506 [D-Arg127	180	55	80.9	22	4	AAB91299	AAB91299 Actrial-na
108	55	80.9	20	2	AAR36942	Aar36942 ANVP #6.	181	55	80.9	22	4	AAB45741	AAB45741 Human C-L
109	55	80.9	20	2	AAR40500	Aar40500 [D-Arg126	182	55	80.9	22	4	AAB12440	AAB12440 Chicken C
110	55	80.9	20	2	AAR40574	Aar40574 [Phe134]r	183	55	80.9	22	4	AAB12433	AAB12433 Frog atril
111	55	80.9	20	2	AAR40569	Aar40569 [N1e133]r	184	55	80.9	22	4	AAB12439	AAB12439 C-type na
112	55	80.9	20	2	AAR40409	Aar40409 [D-Cys130	185	55	80.9	22	4	AAB12441	AAB12441 Frog C-cy
113	55	80.9	20	2	AAR40393	Aar40393 hANVP (126	186	55	80.9	22	4	AAB70811	AAB70811 Human nat
114	55	80.9	20	2	AAR40694	Aar40694 [N1e134]h	187	55	80.9	22	5	AAB98202	AAB98202 Human C-L
115	55	80.9	20	2	AAR40392	Aar40392 hANVP (126	188	55	80.9	22	6	ADAO0766	ADAO0766 Human nat
116	55	80.9	20	2	AAR40396	Aar40396 hANVP (127	189	55	80.9	22	6	ABU63217	ABU63217 N-terminu
117	55	80.9	20	2	AAR40480	Aar40480 [D-Cys146	190	55	80.9	22	6	ABU63218	ABU63218 Human C-L
118	55	80.9	21	1	AAP60769	Aap60769 Rat actrio	191	55	80.9	22	8	AD122343	AD122343 Natriurec
119	55	80.9	21	1	AAP71371	Aap71371 Antihyper	192	55	80.9	22	8	AD122348	AD122348 Natriurec
120	55	80.9	21	1	AAR36962	Aar36962 ANVP #26.	193	55	80.9	22	8	AD122353	AD122353 Natriurec
121	55	80.9	21	2	AAR40603	Aar40603 [Arg129]h	194	55	80.9	22	8	AD122347	AD122347 Natriurec
122	55	80.9	21	2	AAR40607	Aar40607 [Arg128]r	195	55	80.9	22	8	AD122344	AD122344 Natriurec
123	55	80.9	21	2	AAR40594	Aar40594 [Arg128]r	196	55	80.9	22	8	ADP49287	ADP49287 Natriurec
124	55	80.9	21	2	AAR40649	Aar40649 [D-Arg128]r	197	55	80.9	22	8	AD122343	AD122343 Natriurec
125	55	80.9	21	2	AAR40638	Aar40638 [Arg128]r	198	55	80.9	22	9	ADW08064	ADW08064 Human ald
126	55	80.9	21	2	AAR40641	Aar40641 [Arg129]r	199	55	80.9	22	9	ADY62996	ADY62996 Human bra
127	55	80.9	21	2	AAR40647	Aar40647 [Arg129]r	200	55	80.9	22	9	ADY62995	ADY62995 Human C-L
128	55	80.9	21	2	AAR40610	Aar40610 [Arg129]r	201	55	80.9	23	1	AAP60770	Aap60770 Rat actrio
129	55	80.9	21	2	AAR40652	Aar40652 [D-Arg129	202	55	80.9	23	1	AAP71131	AAP71131 Sequence
130	55	80.9	21	4	AAB91307	Aab91307 Actrial-na	203	55	80.9	23	1	AAP71447	AAP71447 Natriurec
131	55	80.9	22	1	AAP50904	Aap50904 Sequence	204	55	80.9	23	1	AAP70962	AAP70962 Sequence
132	55	80.9	22	1	AAP71374	Aap71374 Antihyper	205	55	80.9	23	1	AAP82915	AAP82915 4-Fluoro-
133	55	80.9	22	1	AAP83168	Aap83168 Actrial Na	206	55	80.9	23	1	AAP82684	AAP82684 Alpha-hum
134	55	80.9	22	1	AAP83177	Aap83177 Actrial Na	207	55	80.9	23	1	AAP82983	AAP82983 Alpha-hum
135	55	80.9	22	1	AAP82882	Aap82882 Human Actr	208	55	80.9	23	1	AAP82984	AAP82984 CNP analo
136	55	80.9	22	2	AAR14792	Aar14792 C-type na	209	55	80.9	23	2	AAR25948	AAR25948 CNP analo
137	55	80.9	22	2	AAR25712	Aar25712 Actrial na	210	55	80.9	23	2	AAR25951	AAR25951 CNP analo
138	55	80.9	22	2	AAR29774	Aar29774 Actrial na	211	55	80.9	23	2	AAR36941	AAR36941 ANVP #5.
139	55	80.9	22	2	AAR25705	Aar25705 Actrial na	212	55	80.9	23	2	AAR36969	AAR36969 ANVP #33.
140	55	80.9	22	2	AAR29773	Aar29773 Actrial na	213	55	80.9	23	2	AAR36974	Aar36974 ANVP #38.
141	55	80.9	22	2	AAR25415	Aar25415 Actrial na	214	55	80.9	23	2	AAR40609	AAR40609 [Arg129]r
142	55	80.9	22	2	AAR24330	Aar24330 Brain pep	215	55	80.9	23	2	AAR40688	AAR40688 [N1e133]r
143	55	80.9	22	2	AAR29721	Aar29721 CNP analo	216	55	80.9	23	2	AAR40487	Aar40487 [D-Asn147
144	55	80.9	22	2	AAR29722	Aar29722 CNP analo	217	55	80.9	23	2	AAR40573	Aar40573 [Phe134]r
145	55	80.9	22	2	AAR29730	Aar29730 CNP analo	218	55	80.9	23	2	AAR40645	Aar40645 [Arg129]r
146	55	80.9	22	2	AAR29914	Aar29914 CNP analo	219	55	80.9	23	2	AAR36976	AAR36976 ANVP #40.
147	55	80.9	22	2	AAR29731	Aar29731 CNP analo	220	55	80.9	23	2	AAR36960	AAR36960 ANVP #31.
148	55	80.9	22	2	AAR29916	Aar29916 CNP analo	221	55	80.9	23	2	AAR36967	AAR36967 ANVP #31.
149	55	80.9	22	2	AAR25954	Aar25954 CNP analo	222	55	80.9	23	2	AAR40395	AAR40395 hANVP (127
150	55	80.9	22	2	AAR25955	Aar25955 CNP analo	223	55	80.9	23	2	AAR40473	Aar40473 [D-Cys145
151	55	80.9	22	2	AAR25956	Aar25956 CNP analo	224	55	80.9	23	2	AAR40499	Aar40499 [D-Arg126
152	55	80.9	22	2	AAR29726	Aar29726 CNP analo	225	55	80.9	23	2	AAR40640	AAR40640 [Arg129]r
153	55	80.9	22	2	AAR29915	Aar29915 CNP analo	226	55	80.9	23	2	AAR36958	AAR36958 ANVP #22.
154	55	80.9	22	2	AAR29723	Aar29723 CNP analo	227	55	80.9	23	2	AAR36972	AAR36972 ANVP #36
155	55	80.9	22	2	AAR29729	Aar29729 CNP analo	228	55	80.9	23	2	AAR40394	AAR40394 hANVP (127
156	55	80.9	22	2	AAR29918	Aar29918 CNP analo	229	55	80.9	23	2	AAR36971	AAR36971 ANVP #35.
157	55	80.9	22	2	AAR29720	Aar29720 CNP analo	230	55	80.9	23	2	AAR40479	AAR40479 [D-Cys146
158	55	80.9	22	2	AAR29724	Aar29724 CNP analo	231	55	80.9	23	2	AAR40482	AAR40482 [D-Ser148
159	55	80.9	22	2	AAR29917	Aar29917 CNP analo	232	55	80.9	23	2	AAR40591	AAR40591 [Arg128]r
160	55	80.9	22	2	AAR25953	Aar25953 CNP analo	233	55	80.9	23	2	AAR36977	AAR36977 ANVP #41.
161	55	80.9	22	2	AAR21589	Aar21589 ANP (7-28	234	55	80.9	23	2	AAR40596	AAR40596 [Arg129]h
162	55	80.9	22	2	AAR21588	Aar21588 ANP (7-28	235	55	80.9	23	2	AAR40606	AAR40606 [Arg128]r
163	55	80.9	22	2	AAR32254	Aar32254 Human CNP	236	55	80.9	23	2	AAR40648	AAR40648 [D-Arg128
164	55	80.9	22	2	AAR40602	Aar40602 [Arg129]h	237	55	80.9	23	2	AAR36965	AAR36965 ANVP #29.
165	55	80.9	22	2	AAR40644	Aar40644 [Arg128]r	238	55	80.9	23	2	AAR36966	AAR36966 ANVP #30.
166	55	80.9	22	2	AAR40646	Aar40646 [Arg129]r	239	55	80.9	23	2	AAR40599	AAR40599 [Arg128]r
167	55	80.9	22	2	AAR40597	Aar40597 [Arg129]h	240	55	80.9	23	2	AAR40651	AAR40651 [D-Arg129
168	55	80.9	22	2	AAR40592	Aar40592 [Arg128]r	241	55	80.9	23	2	AAR40408	AAR40408 [D-Cys130
169	55	80.9	22	2	AAR36961	Aar36961 ANVP #25.	242	55	80.9	23	2	AAR40608	AAR40608 [Arg128]r
170	55	80.9	22	2	AAR40598	Aar40598 [Arg129]h	243	55	80.9	23	2	AAR40505	AAR40505 [D-Arg127

244	55	80.9	23	2	AAR40637	[Arg128] I	317	55	80.9	25	2	AAR40443	[D-Ser141
245	55	80.9	23	2	AAR40643	Aar40643 [Arg128] I	318	55	80.9	25	2	AAR40488	[D-Ser148
246	55	80.9	23	2	AAR40655	Aar40655 [Nle134]h	319	55	80.9	25	2	AAR40508	[D-Ser128
247	55	80.9	23	2	AAR36973	ANVP #37.	320	55	80.9	25	2	AAR36937	ANVP #1.
248	55	80.9	23	2	AAR40593	Aar40593 [Arg139]r	321	55	80.9	25	2	AAR40404	[D-Cys130
249	55	80.9	23	2	AAR40612	Aar40612 [Arg128]l	322	55	80.9	25	2	AAR40441	[D-Ala139
250	55	80.9	23	4	AAB91308	Aab91308 Actrial-na	323	55	80.9	25	2	AAR40475	[D-Cys146
251	55	80.9	23	4	AAB91348	Aab91348 C-type na	324	55	80.9	25	2	AAR40482	Aar40482 [D-Abn147
252	55	80.9	23	4	AAB91305	Aab91305 Actrial-na	325	55	80.9	25	2	AAR40388	Aar40388 hANVP (127
253	55	80.9	24	1	AAp50848	AAp50848 Sequence	326	55	80.9	25	2	AAR40405	[D-Cys130
254	55	80.9	24	1	AAp51230	AAp51230 Sequence	327	55	80.9	25	2	AAR40410	[D-Phe130
255	55	80.9	24	1	AAp60771	AAp60771 Rat actrio	328	55	80.9	25	2	AAR40484	Aar40484 [D-Abn147
256	55	80.9	24	1	AAp70964	AAp70964 Sequence	329	55	80.9	25	2	AAR40489	Aar40489 [D-Abn148
257	55	80.9	24	1	AAp94848	AAp94848 Sequence	330	55	80.9	25	2	AAR40494	Aar40494 [D-Phe147
258	55	80.9	24	1	AAp94850	AAp94850 Sequence	331	55	80.9	25	2	AAp40507	[D-Ser127
259	55	80.9	24	2	AAp404102	AAp404102 Intraneaa	332	55	80.9	25	2	AAp40746	[D-Abn136
260	55	80.9	24	2	AAp36940	Aar36940 ANVP #4.	333	55	80.9	25	2	AAp36939	ANVP #3.
261	55	80.9	24	2	AAp40389	AAp40389 hANVP (127	334	55	80.9	25	2	AAp36944	ANVP #8.
262	55	80.9	24	2	AAp40485	Aar40485 [D-Abn147	335	55	80.9	25	2	AAp36945	ANVP #9.
263	55	80.9	24	2	AAp40490	Aar40490 [D-Ser148	336	55	80.9	25	2	AAp36953	ANVP #17.
264	55	80.9	24	2	AAp40390	Aar40390 hANVP (127	337	55	80.9	25	2	AAp40745	[D-Abn135
265	55	80.9	24	2	AAp40401	Aar40401 [D-Cys129	338	55	80.9	25	2	AAp40398	[D-Cys129
266	55	80.9	24	2	AAp40686	Aar40686 [Nle133]r	339	55	80.9	25	2	AAp36955	ANVP #19.
267	55	80.9	24	2	AAp40692	Aar40692 [Nle134]h	340	55	80.9	25	2	AAp40399	[D-Cys129
268	55	80.9	24	2	AAp40478	Aar40478 [D-Cys146	341	55	80.9	25	2	AAp40743	[D-Ile137
269	55	80.9	24	2	AAp40503	Aar40503 [D-Arg127	342	55	80.9	25	2	AAp36946	ANVP #10.
270	55	80.9	24	2	AAp40400	Aar40400 [D-Cys129	343	55	80.9	25	2	AAp40691	[Nle134]h
271	55	80.9	24	2	AAp40486	Aar40486 [D-Abn147	344	55	80.9	25	2	AAp40470	[D-Cys145
272	55	80.9	24	2	AAp40472	Aar40472 [D-Cys145	345	55	80.9	25	2	AAp40493	[D-Phe148
273	55	80.9	24	2	AAp40693	Aar40693 [Nle134]h	346	55	80.9	25	2	AAp40495	[D-Arg126
274	55	80.9	24	2	AAp40406	Aar40406 [D-Cys130	347	55	80.9	25	2	AAp40711	[Lys134]f
275	55	80.9	24	2	AAp36938	Aar36938 ANVP #2.	348	55	80.9	25	2	AAp40744	[D-Ile138
276	55	80.9	24	2	AAp40391	Aar40391 hANVP (126	349	55	80.9	25	2	AAp36948	ANVP #12.
277	55	80.9	24	2	AAp40477	Aar40477 [D-Cys146	350	55	80.9	25	2	AAp40481	[D-Abn146
278	55	80.9	24	2	AAp40471	Aar40471 [D-Cys145	351	55	80.9	25	2	AAp40483	[D-Abn147
279	55	80.9	24	2	AAp40687	Aar40687 [Nle133]r	352	55	80.9	25	2	AAp40496	[D-Arg126
280	55	80.9	24	2	AAp40407	Aar40407 [D-Cys130	353	55	80.9	25	2	AAp40690	[Nle134]f
281	55	80.9	24	2	AAp40491	Aar40491 [D-Ser148	354	55	80.9	25	2	AAp40748	[D-Ala140
282	55	80.9	24	2	AAp40498	Aar40498 [D-Arg126	355	55	80.9	25	2	AAp40476	[D-Cys146
283	55	80.9	24	2	AAp40504	Aar40504 [D-Arg127	356	55	80.9	25	2	AAp40502	[D-Arg127
284	55	80.9	24	2	AAp40402	Aar40402 [D-Cys129	357	55	80.9	25	2	AAp42952	Polypepti
285	55	80.9	24	2	AAp40571	Aar40571 [Phe134]r	358	55	80.9	25	4	AAB91312	Aab91312 Actrial-na
286	55	80.9	24	2	AAp40572	Aar40572 [Phe134]r	359	55	80.9	25	4	AAB91304	Aab91304 Actrial-na
287	55	80.9	24	2	AAp40497	Aar40497 [D-Arg126	360	55	80.9	25	8	ADL73465	ADL73465 Actrial-na
288	55	80.9	24	4	AAp91297	Aab91297 Actrial-na	361	55	80.9	26	1	AAp50113	AAp50113 Biologica
289	55	80.9	24	4	AAp91311	Aab91311 Actrial-na	362	55	80.9	26	1	AAp51106	AAp51106 Sequence
290	55	80.9	24	4	AAp91329	Aab91329 Actrial-na	363	55	80.9	26	1	AAp60807	AAp60807 Actrial na
291	55	80.9	24	4	AAp91326	Aab91326 Actrial-na	364	55	80.9	26	1	AAp71129	AAp71129 Sequence
292	55	80.9	24	4	AAp91309	Aab91309 Actrial-na	365	55	80.9	26	1	AAp71130	AAp71130 Sequence
293	55	80.9	24	8	ADL22345	ADL22345 Nactriuret	366	55	80.9	26	1	AAp70966	AAp70966 Sequence
294	55	80.9	24	8	ADL22346	ADL22346 Nactriuret	367	55	80.9	26	2	AAp40816	AAp40816 Peptide w
295	55	80.9	25	1	AAp51233	AAp51233 Sequence	368	55	80.9	26	2	AAp08309	Aar08309 Chelated
296	55	80.9	25	1	AAp51236	AAp51236 Sequence	369	55	80.9	26	2	AAp04812	AAp04812 Peptide a
297	55	80.9	25	1	AAp51229	AAp51229 Sequence	370	55	80.9	26	2	AAp21586	AAp21586 ANF (3-28
298	55	80.9	25	1	AAp51232	AAp51232 Sequence	371	55	80.9	26	4	AAB91302	Aab91302 Actrial-na
299	55	80.9	25	1	AAp61016	AAp61016 Alpha-fra	372	55	80.9	26	4	AAB91335	Aab91335 Brain nat
300	55	80.9	25	1	AAp61025	AAp61025 Peptide h	373	55	80.9	26	4	AAB91303	Aab91303 Actrial-na
301	55	80.9	25	1	AAp71467	AAp71467 Sequence	374	55	80.9	27	1	AAp60084	AAp60084 Sequence
302	55	80.9	25	2	AAp40456	Aar40456 [D-Leu143	375	55	80.9	27	1	AAp71464	AAp71464 Sequence
303	55	80.9	25	2	AAp40510	Aar40510 [D-Ser129	376	55	80.9	27	1	AAp70970	AAp70970 Sequence
304	55	80.9	25	2	AAp40685	Aar40685 [Nle133]r	377	55	80.9	27	2	AAp11853	AAp11853 Bel natrri
305	55	80.9	25	2	AAp36952	ANVP #16.	378	55	80.9	27	2	AAp25950	AAp25950 CNP analo
306	55	80.9	25	2	AAp36956	ANVP #20.	379	55	80.9	27	2	AAp25949	AAp25949 CNP analo
307	55	80.9	25	2	AAp40501	Aar40501 [D-Arg127	380	55	80.9	27	2	AAp62358	Aar62358 Vasonatrri
308	55	80.9	25	2	AAp40509	Aar40509 [Phe134]r	381	55	80.9	27	2	AAp62357	AAp62357 Generic n
309	55	80.9	25	2	AAp40569	Aar40569 [Phe134]r	382	55	80.9	27	4	AAB91306	Aab91306 Actrial-na
310	55	80.9	25	2	AAp40570	Aar40570 [Phe134]r	383	55	80.9	27	4	AAB91315	Aab91315 Actrial-na
311	55	80.9	25	2	AAp40710	Aar40710 [Lys133]r	384	55	80.9	27	4	AAB91325	Aab91325 Actrial-na
312	55	80.9	25	2	AAp40684	Aar40684 [Nle133]r	385	55	80.9	27	4	AAB91347	Aab91347 C-type na
313	55	80.9	25	2	AAp40742	ID-Ile134	386	55	80.9	27	8	ADL92008	ADL92008 Vasonatrri
314	55	80.9	25	2	AAp36950	ANVP #14.	387	55	80.9	27	8	ADL91962	ADL91962 Vasonatrri
315	55	80.9	25	2	AAp36951	ANVP #15.	388	55	80.9	27	8	ADN03415	ADN03415 Exemplary
316	55	80.9	25	2	AAp40387	hANVP (126	389	55	80.9	27	8	ADR442250	ADR442250 Vasonatrri

390	55	80.9	28	1	AAp50048	Cardionat	463	55	80.9	28	8	ADR42125	Adt42125	Actrial Na
391	55	80.9	28	1	AAp50172	Sequence	464	55	80.9	28	8	ADP92528	Adp92528	Cyclic pe
392	55	80.9	28	1	AAp50118	Sequence	465	55	80.9	28	8	ADV86889	Adv86889	Rat alpha
393	55	80.9	28	1	AAp60076	Sequence	466	55	80.9	28	9	ADV86888	Adv86888	Human alp
394	55	80.9	28	1	AAp61015	Alpha-Ira	467	55	80.9	28	9	ADW08063	Adw08063	Human bra
395	55	80.9	28	1	AAp61400	Alpha-hum	468	55	80.9	28	9	ADW95864	Adw95864	Human actr
396	55	80.9	28	1	AAp71696	Actrial na	469	55	80.9	28	9	ADW45305	Adw45305	Human fus
397	55	80.9	28	1	AAp71202	Lysine fr	470	55	80.9	28	9	ADV62992	Adv62992	Human actr
398	55	80.9	28	1	AAp70655	Sequence	471	55	80.9	29	2	AAp04817	Ap04817	Peptide w
399	55	80.9	28	1	AAp71419	7,23-Cys(472	55	80.9	29	2	AAp04814	Ap04814	Peptide a
400	55	80.9	28	1	AAp82005	Diuretic	473	55	80.9	29	2	AAp13079	Ap13079	Tetradeca
401	55	80.9	28	1	AAp91314	Sequence	474	55	80.9	29	2	AAp13080	Ap13080	Tetradeca
402	55	80.9	28	1	AAp91305	Actria	475	55	80.9	29	2	AAp70094	Ap70094	Natriuret
403	55	80.9	28	2	AAp03306	Rat actria	476	55	80.9	29	2	AAp67041	Ap67041	Actrial na
404	55	80.9	28	2	AAp04819	Peptide w	477	55	80.9	29	4	AAp61289	Ap61289	Actrial na
405	55	80.9	28	2	AAp04815	Peptide w	478	55	80.9	29	4	AAp12438	Ap12438	Chicken b
406	55	80.9	28	2	AAp05859	Actrial na	479	55	80.9	29	8	ADL22335	Adl22335	Natriuret
407	55	80.9	28	2	AAp04941	Actrial na	480	55	80.9	29	9	ADV86895	Adv86895	NP peptid
408	55	80.9	28	2	AAp03415	N-termina	481	55	80.9	31	1	AAp51105	Ap51105	Sequence
409	55	80.9	28	2	AAp04811	Peptide a	482	55	80.9	31	1	AAp71465	Ap71465	Sequence
410	55	80.9	28	2	AAp03302	Sequence	483	55	80.9	31	2	AAp31170	Ap31170	Human psh
411	55	80.9	28	2	AAp29725	CNP analo	484	55	80.9	31	4	AAp71941	Ap71941	Ubiquitin
412	55	80.9	28	2	AAp40042	Leu-(Gly)	485	55	80.9	32	1	AAp51104	Ap51104	Sequence
413	55	80.9	28	2	AAp37109	Protected	486	55	80.9	32	1	AAp71466	Ap71466	Sequence
414	55	80.9	28	2	AAp37110	human actr	487	55	80.9	32	1	AAp71463	Ap71463	Sequence
415	55	80.9	28	2	AAp87093	Actrial na	488	55	80.9	32	1	AAp80388	Ap80388	Sequence
416	55	80.9	28	2	AAp11624	Target pe	489	55	80.9	32	2	AAp88516	Ap88516	Urodlacti
417	55	80.9	28	2	AAp70088	Alpha rat	490	55	80.9	32	2	AAp70092	Ap70092	Brain nat
418	55	80.9	28	2	AAp70087	Alpha hum	491	55	80.9	32	2	AAp67039	Ap67039	Actrial na
419	55	80.9	28	2	AAp51308	Human A-t	492	55	80.9	32	2	AAp51301	Ap51301	Canine B-
420	55	80.9	28	2	AAp62656	Human actr	493	55	80.9	32	2	AAp51302	Ap51302	Porcine B-
421	55	80.9	28	2	AAp93094	Natriuret	494	55	80.9	32	3	AAp80221	Ap80221	Canine B-
422	55	80.9	28	3	AAp80216	Human A-t	495	55	80.9	32	3	AAp80222	Ap80222	Porcine B
423	55	80.9	28	3	AAp98488	Pep 23 us	496	55	80.9	32	4	AAp91314	Ap91314	Actrial na
424	55	80.9	28	3	AAp59033	Sequence	497	55	80.9	32	4	AAp91331	Ap91331	Actrial na
425	55	80.9	28	3	AAp02102	Alpha-hum	498	55	80.9	32	4	AAp91337	Ap91337	Brain nat
426	55	80.9	28	4	AAp82549	Human actr	499	55	80.9	32	4	AAp91328	Ap91328	Brain nat
427	55	80.9	28	4	AAp45841	Nucleic a	500	55	80.9	32	4	AAp91336	Ap91336	Brain nat
428	55	80.9	28	4	AAp81020	Actrial na	501	55	80.9	32	4	AAp45736	Ap45736	Canine BN
429	55	80.9	28	4	AAp91319	Actrial na	502	55	80.9	32	4	AAp12436	Ap12436	Pig Brain
430	55	80.9	28	4	AAp91310	Actrial-na	503	55	80.9	32	4	AAp70812	Ap70812	Humanuro
431	55	80.9	28	4	AAp91300	Actrial-na	504	55	80.9	32	6	ADp00764	Adp00764	Human nat
432	55	80.9	28	4	AAp45740	Human A-t	505	55	80.9	32	7	ADp17063	Adp17063	Human alb
433	55	80.9	28	4	AAp04278	Nuclear 1	506	55	80.9	32	8	ADL22338	Adl22338	Natriuret
434	55	80.9	28	4	AAp12432	Rat actria	507	55	80.9	32	8	ADL22340	Adl22340	Natriuret
435	55	80.9	28	4	AAp12431	Human actr	508	55	80.9	32	8	ADL22339	Adl22339	Natriuret
436	55	80.9	28	4	AAp70809	Human nat	509	55	80.9	32	8	ADp49281	Adp49281	Natriuret
437	55	80.9	28	5	AAp85983	Modified	510	55	80.9	32	8	ADp49276	Adp49276	Natriuret
438	55	80.9	28	5	AAp680710	Human ANP	511	55	80.9	32	8	ADp49301	Adp49301	Natriuret
439	55	80.9	28	5	AAp988204	Human actr	512	55	80.9	32	9	ADp49301	Adp49301	Beta BNP
440	55	80.9	28	6	ADp00783	Human nat	513	55	80.9	33	1	AAp51103	Ap51103	Sequence
441	55	80.9	28	6	ADp00825	Human hAN	514	55	80.9	33	1	AAp50112	Ap50112	Biologica
442	55	80.9	28	6	ADp00771	Rat natri	515	55	80.9	35	1	AAp60806	Ap60806	Actrial na
443	55	80.9	28	6	ADp00822	Human hAN	516	55	80.9	35	1	AAp61765	Ap61765	Sequence
444	55	80.9	28	6	ADp00823	Human hAN	517	55	80.9	35	1	AAp60270	Ap60270	Sequence
445	55	80.9	28	6	ADp00785	Rat natri	518	55	80.9	35	2	AAp08327	Ap08327	Chelated
446	55	80.9	28	6	ABp63214	Human actr	519	55	80.9	35	2	AAp08328	Ap08328	Chelated
447	55	80.9	28	7	ADp17067	Human alb	520	55	80.9	35	2	AAp06352	Ap06352	Actrial na
448	55	80.9	28	8	ADp192004	Actrial na	521	55	80.9	35	2	AAp06353	Ap06353	Actrial na
449	55	80.9	28	8	ADL22342	Natriuret	522	55	80.9	37	2	AAp25986	Ap25986	Ventriculu
450	55	80.9	28	8	ADL22349	Natriuret	523	55	80.9	37	2	AAp65450	Ap65450	Lebectin d
451	55	80.9	28	8	ADL22337	Natriuret	524	55	80.9	37	4	AAp882544	Ap882544	Human C-t
452	55	80.9	28	8	ADL22334	Natriuret	525	55	80.9	37	6	ABp63211	Ap63211	Chimeric
453	55	80.9	28	8	ADL22331	Natriuret	526	55	80.9	37	9	ADp62989	Adp62989	Natriuret
454	55	80.9	28	8	ADL22333	Natriuret	527	55	80.9	38	2	AAp65449	Ap65449	Lebectin d
455	55	80.9	28	8	ADL22330	Natriuret	528	55	80.9	40	2	AAp21945	Ap21945	Fusion pr
456	55	80.9	28	8	ADL22332	Natriuret	529	55	80.9	42	2	AAp13323	Ap13323	Alpba-hum
457	55	80.9	28	8	ADp03290	Human actr	530	55	80.9	43	1	AAp60078	Ap60078	Sequence
458	55	80.9	28	8	ADp18406	Neurogene	531	55	80.9	43	1	AAp81211	Ap81211	Alpba-hum
459	55	80.9	28	8	ADp18427	Neurogene	532	55	80.9	45	1	AAp70093	Ap70093	Brain nat
460	55	80.9	28	8	ADp49288	Natriuret	533	55	80.9	45	2	AAp51304	Ap51304	Mouse B-t
461	55	80.9	28	8	ADp49288	Natriuret	534	55	80.9	45	2	AAp51303	Ap51303	Rat B-tyr
462	55	80.9	28	8	ADp26469	Post-tran	535	55	80.9	45	2	AAp51303	Ap51303	Rat B-tyr

536	55	80.9	45	3	AAy80224	609	55	80.9	131	7	ADP93294	Ad93294	Pig prepr
537	55	80.9	45	3	AAy80223	610	55	80.9	131	8	ADM41432	Adm41432	Pig brain
538	55	80.9	45	4	AAy81334	611	55	80.9	133	1	AAp60080	App60080	Sequence
539	55	80.9	45	4	AAy81338	612	55	80.9	136	2	AAr36935	Aar36935	Human pre
540	55	80.9	45	4	AAy812437	613	55	80.9	140	6	AAr05669	Aar05669	Gamma-chl
541	55	80.9	45	4	ADy86894	614	55	80.9	140	6	ADa09507	Ada09507	Canine br
542	55	80.9	46	2	AAw65444	615	55	80.9	140	8	ADM41417	Adm41417	Canine br
543	55	80.9	48	1	AAp50115	616	55	80.9	144	2	AAr21677	Aar21677	Beta-gal
544	55	80.9	53	2	AAw16490	617	55	80.9	144	2	AAr21676	Aar21676	Beta-gal
545	55	80.9	53	2	AAw121991	618	55	80.9	147	2	AAr03301	Aar03301	Sequence
546	55	80.9	53	2	AD124859	619	55	80.9	150	1	AAp51239	App51239	Sequence
547	55	80.9	53	4	AAy81344	620	55	80.9	150	1	AAp51241	App51241	Sequence
548	55	80.9	53	4	AAy81343	621	55	80.9	151	1	AAp50050	App50050	Cardioidl
549	55	80.9	53	8	AD192007	622	55	80.9	151	1	AAp50036	App50036	Sequence
550	55	80.9	56	4	AAy81313	623	55	80.9	151	1	AAp70629	App70629	Sequence
551	55	80.9	62	1	AAp60165	624	55	80.9	151	2	AAr36934	Aar36934	Human pre
552	55	80.9	71	1	AAp51102	625	55	80.9	151	2	AAw98193	Aaw98193	Human atr
553	55	80.9	73	1	AAp51107	626	55	80.9	151	8	ADM41415	Adm41415	Human atr
554	55	80.9	88	1	AAp50493	627	55	80.9	151	8	ADM41343	Adm41343	Human pre
555	55	80.9	101	3	AAy80531	628	55	80.9	151	8	ADr75285	Adr75285	Human atr
556	55	80.9	103	3	AAy810489	629	55	80.9	151	8	ADU05014	Adu05014	Amino aci
557	55	80.9	103	3	ADW46288	630	55	80.9	151	8	ADU04663	Adu04663	Human atr
558	55	80.9	103	9	ADW46287	631	55	80.9	151	8	ADY34280	Ady34280	Human atr
559	55	80.9	103	9	ADW46291	632	55	80.9	151	9	AAy80582	Aay80582	Human atr
560	55	80.9	103	9	ADW46290	633	55	80.9	152	1	AAp51242	App51242	Sequence
561	55	80.9	103	9	ADW46292	634	55	80.9	152	1	AAp60325	App60325	Gamma-ra
562	55	80.9	103	9	ADW46289	635	55	80.9	152	2	AAr36936	Aar36936	Rat pre-p
563	55	80.9	111	1	AAp50565	636	55	80.9	152	2	AAw98191	Aaw98191	Rat atria
564	55	80.9	115	1	AAy82911	637	55	80.9	152	8	ADP86020	Adp86020	Truncated
565	55	80.9	116	1	AAp50102	638	55	80.9	152	8	ADM41429	Adm41429	Bovine at
566	55	80.9	118	2	AAy80532	639	55	80.9	152	8	ADM41352	Adm41352	Murine pr
567	55	80.9	120	2	AAy84670	640	55	80.9	153	7	ADP44952	Adp44952	Human atr
568	55	80.9	120	2	AAy84669	641	55	80.9	153	7	ADP86021	Adp86021	Truncated
569	55	80.9	121	2	AAr10973	642	55	80.9	161	5	AAy83328	Aay83328	Human ORF
570	55	80.9	121	2	AAy84668	643	55	80.9	168	4	AAy81019	Aay81019	Interleuk
571	55	80.9	121	7	AAy84667	644	55	80.9	169	9	ADW08082	Adw08082	Dog brain
572	55	80.9	121	7	ADP93295	645	55	80.9	196	7	ADP44937	Adp44937	Heloderna
573	55	80.9	121	8	ADM41431	646	55	80.9	198	5	AAy869270	Aay869270	Human pol
574	55	80.9	121	8	ADM41430	647	55	80.9	240	2	AAr05425	Aar05425	Amino aci
575	55	80.9	122	2	AAy86282	648	55	80.9	241	1	AAp92070	App92070	Sequence
576	55	80.9	125	1	AAy86286	649	55	80.9	265	6	AAy86118	Aay86118	Bothrops
577	55	80.9	126	1	AAp50037	650	55	80.9	340	3	AAO20104	Aao20104	Gene-9 a1
578	55	80.9	126	1	AAp51240	651	55	80.9	637	9	AAy845218	Aay845218	Human ser
579	55	80.9	126	1	AAp60017	652	54	79.4	17	5	AAy898206	Aay898206	Human deg
580	55	80.9	126	2	AAy800582	653	54	79.4	17	5	AAy898256	Aay898256	Human C-c
581	55	80.9	126	2	AAy829912	654	54	79.4	17	5	AAy898253	Aay898253	Human C-c
582	55	80.9	126	2	AAy829913	655	54	79.4	17	5	AAy898258	Aay898258	Human C-c
583	55	80.9	126	2	AAy820182	656	54	79.4	20	2	AAy898266	Aay898266	Human C-c
584	55	80.9	126	2	AAy822188	657	54	79.4	20	2	AAy840580	Aay840580	Human C-c
585	55	80.9	126	2	AAy822361	658	54	79.4	20	2	AAy840586	Aay840586	Human C-c
586	55	80.9	126	2	AAy820074	659	54	79.4	22	2	AAy825711	Aay825711	Human C-c
587	55	80.9	126	2	AAy816491	660	54	79.4	22	2	AAy821828	Aay821828	Human C-c
588	55	80.9	126	2	AAy821990	661	54	79.4	23	2	AAy840585	Aay840585	Human C-c
589	55	80.9	126	2	AAy834533	662	54	79.4	23	2	AAy836978	Aay836978	Human C-c
590	55	80.9	126	3	AAy810488	663	54	79.4	23	2	AAy840579	Aay840579	Human C-c
591	55	80.9	126	3	AAy8084726	664	54	79.4	24	2	AAy840584	Aay840584	Human C-c
592	55	80.9	126	3	AAy8084725	665	54	79.4	24	2	AAy840578	Aay840578	Human C-c
593	55	80.9	126	3	AAy875286	666	54	79.4	24	2	AAy840577	Aay840577	Human C-c
594	55	80.9	126	3	AAy875284	667	54	79.4	24	2	AAy840583	Aay840583	Human C-c
595	55	80.9	126	3	AAy805015	668	54	79.4	25	1	AAy851234	Aay851234	Human C-c
596	55	80.9	126	3	AAy805013	669	54	79.4	25	1	AAy840582	Aay840582	Human C-c
597	55	80.9	126	3	AAy804662	670	54	79.4	25	2	AAy840576	Aay840576	Human C-c
598	55	80.9	126	3	AAy804664	671	54	79.4	25	2	AAy840581	Aay840581	Human C-c
599	55	80.9	126	3	AAy805863	672	54	79.4	25	2	AAy840575	Aay840575	Human C-c
600	55	80.9	126	3	AAy834279	673	54	79.4	25	2	AAy840439	Aay840439	Human C-c
601	55	80.9	126	3	AAy834281	674	54	79.4	25	2	AAy836957	Aay836957	Human C-c
602	55	80.9	128	1	AAy851238	675	54	79.4	25	2	AAy842954	Aay842954	Human C-c
603	55	80.9	129	3	AAy823576	676	54	79.4	26	2	AAy821587	Aay821587	Human C-c
604	55	80.9	129	3	AAy823576	677	54	79.4	26	2	AAy821587	Aay821587	Human C-c
605	55	80.9	131	2	AAy807342	678	53	77.9	17	5	AAy898252	Aay898252	Human C-c
606	55	80.9	131	2	AAy804084	679	52	76.5	17	5	AAy898250	Aay898250	Human C-c
607	55	80.9	131	2	AAy804086	680	52	76.5	22	2	AAy825708	Aay825708	Human C-c
608	55	80.9	131	2	AAy813325	681	52	76.5	24	1	AAy84851	Aay84851	Human C-c

682	52	76.5	25	2	AAR40713	Aar40713 [Lys137]h	755	50	73.5	24	8	ADL22366	Adl22366 Nactiuret
683	52	76.5	25	2	AAR40712	Aar40712 [Lys136]r	756	50	73.5	24	8	ADL22360	Adl22360 Nactiuret
684	51	75.0	17	1	AAE71037	Aae71037 Peptide w	757	50	73.5	24	8	ADL22363	Adl22363 Nactiuret
685	51	75.0	17	5	ABG98236	Abg98236 Human C-t	758	50	73.5	24	8	ADP49306	Adp49306 Nactiuret
686	51	75.0	17	5	ABG98251	Abg98251 Human C-t	759	50	73.5	25	2	AAR40511	Aar40511 [D-Ala13]
687	51	75.0	22	2	AAR25713	Aar25713 Actrial na	760	50	73.5	25	2	AAR40517	Aar40517 [D-Ala13]
688	51	75.0	23	1	AAE70968	Aae70968 Sequence	761	50	73.5	25	2	AAR40518	Aar40518 [D-Ala13]
689	51	75.0	23	1	AAE70969	Aae70969 Sequence	762	50	73.5	25	2	AAR40557	Aar40557 [D-Ala13]
690	51	75.0	24	1	AAE70963	Aae70963 Sequence	763	50	73.5	25	2	AAR40512	Aar40512 [D-Ala13]
691	51	75.0	24	1	AAE70964	Aae70964 Sequence	764	50	73.5	25	2	AAR40564	Aar40564 [Asn136]h
692	51	75.0	25	2	AAR40741	Aar40741 [Glu136]h	765	50	73.5	25	2	AAR40563	Aar40563 [Asn135]r
693	51	75.0	25	2	AAR40740	Aar40740 [Glu135]r	766	50	73.5	25	2	AAR40558	Aar40558 [Asn135]r
694	51	75.0	25	2	AAR42953	Aar42953 Polypepti	767	50	73.5	25	2	ADL22352	Adl22352 Nactiuret
695	51	75.0	32	2	AAW51274	Aaw51274 Human B-t	768	50	73.5	25	8	ADL22356	Adl22356 Nactiuret
696	51	75.0	32	3	AAE80244	Aae80244 Human B-t	769	50	73.5	25	8	ADL22355	Adl22355 Nactiuret
697	51	75.0	32	3	ABG98210	Abg98210 Human C-t	770	50	73.5	25	8	ADP49282	Adp49282 Nactiuret
698	50	73.5	17	5	ABG98249	Abg98249 Human C-t	771	50	73.5	26	3	AAE67295	Aae67295 Human bra
699	50	73.5	17	5	ABG98254	Abg98254 Human C-t	772	50	73.5	26	6	ABU63216	Abu63216 N-terminu
700	50	73.5	17	5	ABG98238	Abg98238 Human C-t	773	50	73.5	26	8	ADL22357	Adl22357 Nactiuret
701	50	73.5	17	5	ABG98232	Abg98232 Human C-t	774	50	73.5	26	8	ADL22354	Adl22354 Nactiuret
702	50	73.5	17	8	ADL22369	Adl22369 Nactiuret	775	50	73.5	26	8	ADP49303	Adp49303 Nactiuret
703	50	73.5	17	8	ADL22372	Adl22372 Nactiuret	776	50	73.5	26	8	ADP49273	Adp49273 Nactiuret
704	50	73.5	17	8	ADL22373	Adl22373 Nactiuret	777	50	73.5	26	9	ADW45317	Adw45317 Human fus
705	50	73.5	17	8	ADL22370	Adl22370 Nactiuret	778	50	73.5	26	9	ADY62994	Ady62994 Human bra
706	50	73.5	17	8	ADP49292	Adp49292 Nactiuret	779	50	73.5	27	8	ADP49289	Adp49289 Nactiuret
707	50	73.5	17	9	ABE12959	Aeb12959 Human bra	780	50	73.5	27	9	ADW45318	Adw45318 Human fus
708	50	73.5	18	2	AAE40656	Aae40656 [Arg128]l	781	50	73.5	27	9	ADW45367	Adw45367 Human BNP
709	50	73.5	18	2	AAE40671	Aae40671 [Arg129]l	782	50	73.5	28	2	AAE14464	Aae14464 Actrlol na
710	50	73.5	18	2	AAE40659	Aae40659 [Arg129]l	783	50	73.5	28	9	ADW45365	Adw45365 Human BNP
711	50	73.5	18	2	AAE40668	Aae40668 [Arg128]l	784	50	73.5	28	9	ADW45319	Adw45319 Human fus
712	50	73.5	18	8	ADL22374	Adl22374 Nactiuret	785	50	73.5	29	1	AAE70972	Aae70972 Sequence
713	50	73.5	18	8	ADL22371	Adl22371 Nactiuret	786	50	73.5	29	8	ADP49272	Adp49272 Nactiuret
714	50	73.5	19	8	ADP49259	Adp49259 Nactiuret	787	50	73.5	29	8	ADP49302	Adp49302 Nactiuret
715	50	73.5	19	8	ADP49298	Adp49298 Nactiuret	788	50	73.5	29	9	ADW45311	Adw45311 Human fus
716	50	73.5	20	2	AAE40516	Aae40516 [D-Ala13]l	789	50	73.5	29	9	ADP49258	Adp49258 Nactiuret
717	50	73.5	20	2	AAE40582	Aae40582 [D-Ala13]l	790	50	73.5	30	2	AAE49258	Aae49258 Nactiuret
718	50	73.5	20	2	AAE40568	Aae40568 [Asn136]h	791	50	73.5	31	2	AAE34302	Aae34302 Mutated B
719	50	73.5	20	2	AAE40552	Aae40552 [Asn135]r	792	50	73.5	32	2	AAE40861	Aae40861 BNP, 3/19
720	50	73.5	21	2	AAE40687	Aae40687 [Arg128]l	793	50	73.5	32	2	AAE34301	Aae34301 Mutated h
721	50	73.5	21	2	AAE40658	Aae40658 [Arg129]l	794	50	73.5	32	2	AAE36381	Aae36381 Recombina
722	50	73.5	21	2	AAE40673	Aae40673 [Arg128]l	795	50	73.5	32	2	AAW70090	Aaw70090 Brain nat
723	50	73.5	21	2	AAE40670	Aae40670 [Arg129]l	796	50	73.5	32	2	AAW67040	Aaw67040 Brain nat
724	50	73.5	21	2	AAE40655	Aae40655 [Arg128]l	797	50	73.5	32	2	AAW51305	Aaw51305 Human B-t
725	50	73.5	22	1	AAE71038	Aae71038 Peptide w	798	50	73.5	32	2	AAW51278	Aaw51278 Human B-t
726	50	73.5	22	1	AAE40669	Aae40669 [Arg129]l	799	50	73.5	32	2	AAW51280	Aaw51280 Human B-t
727	50	73.5	23	2	AAE40654	Aae40654 [Arg128]l	800	50	73.5	32	3	AAE180250	Aae180250 Human B-t
728	50	73.5	23	2	AAE40666	Aae40666 [Arg129]l	801	50	73.5	32	3	AAE80213	Aae80213 Human B-t
729	50	73.5	23	2	AAE40657	Aae40657 [Arg129]l	802	50	73.5	32	3	AAE80248	Aae80248 Human B-t
730	50	73.5	23	2	AAE40672	Aae40672 [Arg128]l	803	50	73.5	32	4	AAE82550	Aae82550 Human bra
731	50	73.5	23	2	AAE40567	Aae40567 [Asn136]h	804	50	73.5	32	4	AAE91333	Aae91333 Brain nat
732	50	73.5	23	2	AAE40555	Aae40555 [D-Ala13]l	805	50	73.5	32	4	AAE91340	Aae91340 Brain nat
733	50	73.5	23	2	AAE40521	Aae40521 [D-Ala13]l	806	50	73.5	32	4	AAE45739	Aae45739 Human mat
734	50	73.5	23	2	AAE40561	Aae40561 [Asn135]r	807	50	73.5	32	4	AAE12434	Aae12434 Human bra
735	50	73.5	23	2	ADL22365	Adl22365 Nactiuret	808	50	73.5	32	4	AAE70810	Aae70810 Human bra
736	50	73.5	23	8	ADL22362	Adl22362 Nactiuret	809	50	73.5	32	5	ABG98205	Abg98205 Human bra
737	50	73.5	23	8	ADL22364	Adl22364 Nactiuret	810	50	73.5	32	6	ADA00765	Ada00765 Human nat
738	50	73.5	23	8	ADL22361	Adl22361 Nactiuret	811	50	73.5	32	6	ADA00784	Ada00784 Human nat
739	50	73.5	23	8	ADL22359	Adl22359 Nactiuret	812	50	73.5	32	6	ABU63215	Abu63215 Human bra
740	50	73.5	23	8	ADL22358	Adl22358 Nactiuret	813	50	73.5	32	7	ADD55931	Add55931 Human B-t
741	50	73.5	24	1	AAE70967	Aae70967 Sequence	814	50	73.5	32	7	ADP16700	Adp16700 Human act
742	50	73.5	24	1	AAE94852	Aae94852 Sequence	815	50	73.5	32	7	ADP179634	Adp179634 Human bra
743	50	73.5	24	1	AAE93098	Aae93098 Sequence	816	50	73.5	32	8	ADL22376	Adl22376 Nactiuret
744	50	73.5	24	2	AAE40514	Aae40514 [D-Ala13]l	817	50	73.5	32	8	ADL22378	Adl22378 Nactiuret
745	50	73.5	24	2	AAE40565	Aae40565 [Asn136]h	818	50	73.5	32	8	ADL22382	Adl22382 Nactiuret
746	50	73.5	24	2	AAE40519	Aae40519 [D-Ala13]l	819	50	73.5	32	8	ADL22384	Adl22384 Nactiuret
747	50	73.5	24	2	AAE40559	Aae40559 [Asn135]r	820	50	73.5	32	8	ADL22351	Adl22351 Nactiuret
748	50	73.5	24	2	AAE40560	Aae40560 [Asn135]r	821	50	73.5	32	8	ADL22379	Adl22379 Nactiuret
749	50	73.5	24	2	AAE40566	Aae40566 [Asn136]h	822	50	73.5	32	8	ADL22367	Adl22367 Nactiuret
750	50	73.5	24	2	AAE40520	Aae40520 [D-Ala13]l	823	50	73.5	32	8	ADL22386	Adl22386 Nactiuret
751	50	73.5	24	2	AAE37337	Aae37337 Actriopept	824	50	73.5	32	8	ADL22375	Adl22375 Nactiuret
752	50	73.5	24	2	AAE37338	Aae37338 Actriopept	825	50	73.5	32	8	ADN03300	Adn03300 Exemplary
753	50	73.5	24	2	AAE46799	Aae46799 Human bra	826	50	73.5	32	8		
754	50	73.5	24	4	AAE46799	Aae46799 Human bra	827	50	73.5	32	8		

828	50	73.5	32	8	ADP49307	Adp49307	Natriuret	901	50	73.5	175	2	AAR72812	Aar72812	Gamma-IFN
829	50	73.5	32	8	ADP49290	Adp49290	Natriuret	902	50	73.5	197	8	ADM57398	Adm57398	Protein p
830	50	73.5	32	8	ADP49308	Adp49308	Natriuret	903	50	73.5	630	9	ADM45230	Adm45230	Human inv
831	50	73.5	32	8	ADP49291	Adp49291	Natriuret	904	50	73.5	631	9	ADM45231	Adm45231	Human inv
832	50	73.5	32	8	ADP42135	Adp42135	BNP relat	905	50	73.5	632	9	ADM45232	Adm45232	Human inv
833	50	73.5	32	9	ADP46891	Adp46891	Human BNP	906	50	73.5	633	9	ADM45224	Adm45224	Human inv
834	50	73.5	32	9	ADM08061	Adm08061	Human bra	907	50	73.5	641	7	ADP16537	Adp16537	Human alb
835	50	73.5	32	9	ADM95867	Adm95867	Human bra	908	50	73.5	641	9	ADM45226	Adm45226	Human ser
836	50	73.5	32	9	ADM45284	Adm45284	Human fus	909	50	73.5	641	9	ADM45207	Adm45207	Human ser
837	50	73.5	32	9	ADM45314	Adm45314	Human fus	910	50	73.5	661	9	ADM45277	Adm45277	Human ser
838	50	73.5	32	9	ADM45294	Adm45294	Human fus	911	50	73.5	663	9	ADM45280	Adm45280	Human ser
839	50	73.5	32	9	ADM45366	Adm45366	Human BNP	912	50	73.5	665	9	ADM45278	Adm45278	Human ser
840	50	73.5	32	9	ADM45300	Adm45300	Human fus	913	50	73.5	667	9	ADM45223	Adm45223	Human ser
841	50	73.5	32	9	ADM45313	Adm45313	Human bra	914	50	73.5	670	9	ADM45297	Adm45297	Human ser
842	50	73.5	32	9	ADP62993	Adp62993	Human bra	915	50	73.5	673	9	ADM45197	Adm45197	Human ser
843	50	73.5	32	9	AEAS3023	Aeas3023	Protein q	916	50	73.5	673	9	ADM45213	Adm45213	Human ser
844	50	73.5	32	9	AEAB63461	Aeab63461	HUMNATPBP	917	50	73.5	673	9	ADM45227	Adm45227	Human ser
845	50	73.5	32	2	AAR45762	Aar45762	GLU-BNP.	918	50	73.5	719	7	ADP16188	Adp16188	Human alb
846	50	73.5	32	2	AAR35490	Aar35490	Tyr-bBNP.	919	49	72.1	17	1	AAFP71035	Aafp71035	Peptide w
847	50	73.5	33	8	ADL22377	Adl22377	Natriuret	920	49	72.1	17	5	ABG98271	Abg98271	Human C-t
848	50	73.5	33	8	ADL22383	Adl22383	Natriuret	921	49	72.1	17	5	ABG98231	Abg98231	Human C-t
849	50	73.5	33	8	ADL22380	Adl22380	Natriuret	922	49	72.1	17	5	ABG98209	Abg98209	Human C-t
850	50	73.5	33	8	ADL22385	Adl22385	Natriuret	923	49	72.1	17	5	ABG98229	Abg98229	Human C-t
851	50	73.5	33	8	ADL22368	Adl22368	Natriuret	924	49	72.1	17	5	ABG98237	Abg98237	Human C-t
852	50	73.5	33	8	ADP49309	Adp49309	Natriuret	925	49	72.1	17	5	ABG98230	Abg98230	Human C-t
853	50	73.5	33	8	ADP49293	Adp49293	Natriuret	926	49	72.1	18	2	AAR40615	Aar40615	Human C-t
854	50	73.5	34	2	AAR45761	Aar45761	Leader-GL	927	49	72.1	18	2	AAR40662	Aar40662	Human C-t
855	50	73.5	35	4	ABB91330	Abb91330	Actrial-na	928	49	72.1	18	2	AAR40633	Aar40633	Human C-t
856	50	73.5	35	8	ADU79736	Adu79736	Human Bra	929	49	72.1	18	2	AAR40618	Aar40618	Human C-t
857	50	73.5	41	4	AAB82543	Aab82543	Human bra	930	49	72.1	18	2	AAR40665	Aar40665	Human C-t
858	50	73.5	41	6	ABU63210	Abu63210	Chimeric	931	49	72.1	18	2	AAR40636	Aar40636	Human C-t
859	50	73.5	41	9	ADM08080	Adm08080	Human bra	932	49	72.1	20	2	AAR40422	Aar40422	Human C-t
860	50	73.5	41	9	ADY62988	Ady62988	Natriuret	933	49	72.1	20	2	AAR40701	Aar40701	Human C-t
861	50	73.5	42	9	AEAB63459	Aeab63459	HUMNATPBP	934	49	72.1	20	2	AAR40719	Aar40719	Human C-t
862	50	73.5	52	9	ADM45364	Adm45364	Human BNP	935	49	72.1	20	2	AAR40546	Aar40546	Human C-t
863	50	73.5	60	9	ADM08083	Adm08083	Human bra	936	49	72.1	20	2	AAR40462	Aar40462	Human C-t
864	50	73.5	60	9	AEB63460	Aeb63460	HUMNATPBP	937	49	72.1	20	2	AAR40725	Aar40725	Human C-t
865	50	73.5	108	7	ADP93297	Adp93297	Human pro	938	49	72.1	20	2	AAR40534	Aar40534	Human C-t
866	50	73.5	108	8	ADU79633	Adu79633	Human Bra	939	49	72.1	20	2	AAR40540	Aar40540	Human C-t
867	50	73.5	108	8	ADU47364	Adu47364	Human bra	940	49	72.1	20	2	AAR40416	Aar40416	Human C-t
868	50	73.5	108	8	ADU47365	Adu47365	Human bra	941	49	72.1	20	2	AAR40528	Aar40528	Human C-t
869	50	73.5	108	8	ADU32544	Adu32544	Human NT-	942	49	72.1	20	2	AAR40468	Aar40468	Human C-t
870	50	73.5	108	8	ADU30871	Adu30871	Human pro	943	49	72.1	20	2	AAR40707	Aar40707	Human C-t
871	50	73.5	108	8	ADR5282	Adr5282	Human bra	944	49	72.1	21	1	AAR94849	Aar94849	Human C-t
872	50	73.5	108	8	ADS54316	Ads54316	Human B-t	945	49	72.1	21	1	AAR40635	Aar40635	Human C-t
873	50	73.5	108	8	ADU05011	Adu05011	Amino aci	946	49	72.1	21	2	AAR40664	Aar40664	Human C-t
874	50	73.5	108	8	ADU04660	Adu04660	Human bra	947	49	72.1	21	2	AAR40617	Aar40617	Human C-t
875	50	73.5	108	9	ADW95866	Adw95866	Human pro	948	49	72.1	21	2	AAR40661	Aar40661	Human C-t
876	50	73.5	108	9	ADY34277	Ady34277	Human bra	949	49	72.1	21	2	AAR40614	Aar40614	Human C-t
877	50	73.5	108	9	ADZ22717	Adz22717	Human B-t	950	49	72.1	21	2	AAR40632	Aar40632	Human C-t
878	50	73.5	109	4	AB445738	Ab445738	Human BNP	951	49	72.1	22	1	ABP50902	Abp50902	Sequence
879	50	73.5	117	8	ADM57402	Adm57402	Protein p	952	49	72.1	22	1	ABP71372	Abp71372	Antihyper
880	50	73.5	118	6	ABR95183	Abr95183	Human NOV	953	49	72.1	22	2	AAR25743	Aar25743	Actrial na
881	50	73.5	121	8	ADM57400	Adm57400	Protein p	954	49	72.1	22	2	AAR29775	Aar29775	Actrial na
882	50	73.5	129	9	AEB63486	Aeb63486	HUMNATPBP	955	49	72.1	22	2	AAR29776	Aar29776	Actrial na
883	50	73.5	134	2	AAR06603	Aar06603	Human Bra	956	49	72.1	23	2	AAR40527	Aar40527	Human C-t
884	50	73.5	134	2	AAR04087	Aar04087	Protein e	957	49	72.1	23	2	AAR40533	Aar40533	Human C-t
885	50	73.5	134	2	AAAY05325	Aay05325	Human gam	958	49	72.1	23	2	AAR40718	Aar40718	Human C-t
886	50	73.5	134	4	AAAB45735	Aab45735	Human BNP	959	49	72.1	23	2	AAR40700	Aar40700	Human C-t
887	50	73.5	134	8	ADD93293	Add93293	Human BNP	960	49	72.1	23	2	AAR40660	Aar40660	Human C-t
888	50	73.5	134	7	ADP16190	Adp16190	Human pre	961	49	72.1	23	2	AAR40661	Aar40661	Human C-t
889	50	73.5	134	8	ADM41613	Adm41613	Human alb	962	49	72.1	23	2	AAR40556	Aar40556	Human C-t
890	50	73.5	134	8	ADQ30872	Adq30872	Human bra	963	49	72.1	23	2	AAR40724	Aar40724	Human C-t
891	50	73.5	134	8	ADR75283	Adr75283	Human bra	964	49	72.1	23	2	AAR36968	Aar36968	Human C-t
892	50	73.5	134	8	ADU54317	Adu54317	Human B-t	965	49	72.1	23	2	AAR40551	Aar40551	Human C-t
893	50	73.5	134	8	ADU50512	Adu50512	Amino aci	966	49	72.1	23	2	AAR40660	Aar40660	Human C-t
894	50	73.5	134	8	ADU04661	Adu04661	Human bra	967	49	72.1	23	2	AAR40415	Aar40415	Human C-t
895	50	73.5	134	9	ADY34278	Ady34278	Human bra	968	49	72.1	23	2	AAR40634	Aar40634	Human C-t
896	50	73.5	134	9	ADZ22718	Adz22718	Human pre	969	49	72.1	23	2	AAR40663	Aar40663	Human C-t
897	50	73.5	134	9	AEAB63456	Aeab63456	HUMNATPBP	970	49	72.1	23	2	AAR40613	Aar40613	Human C-t
898	50	73.5	143	9	ADM08049	Adm08049	Human bra	971	49	72.1	23	2	AAR40467	Aar40467	Human C-t
899	50	73.5	162	9	ADM08048	Adm08048	Human bra	972	49	72.1	23	2	AAR40539	Aar40539	Human C-t
900	50	73.5	162	9	AEB63457	Aeb63457	HUMNATPBP	973	49	72.1	23	2	AAR40545	Aar40545	Human C-t

```
974 49 72.1 23 2 AAR40421 Aar40421 [D-Ala132
975 49 72.1 23 2 AAR40616 Aar40616 [Arg1291]
976 49 72.1 23 2 AAR40631 Aar40631 [Ser1361h
977 49 72.1 23 2 AAR40706 Aar40706 [Ser1361h
978 49 72.1 23 2 AAR40552 Aar40552 ID-Ala132
979 49 72.1 24 1 AAP50908 Aap50908 Sequence
980 49 72.1 24 2 AAR40544 Aar40544 [D-Cys130
981 49 72.1 24 2 AAR40413 Aar40413 ID-Ala131
982 49 72.1 24 2 AAR40531 Aar40531 ID-Ala132
983 49 72.1 24 2 AAR40550 Aar40550 ID-Ala131
984 49 72.1 24 2 AAR40704 Aar40704 [Ser1361h
985 49 72.1 24 2 AAR40538 Aar40538 ID-Cys129
986 49 72.1 24 2 AAR40716 Aar40716 [Leu1301r
987 49 72.1 24 2 AAR40526 Aar40526 ID-Ala131
988 49 72.1 24 2 AAR40598 Aar40598 [Ser1351r
989 49 72.1 24 2 AAR40723 Aar40723 [Leu1311h
990 49 72.1 24 2 AAR40717 Aar40717 [Leu1301r
991 49 72.1 24 2 AAR40525 Aar40525 ID-Ala131
992 49 72.1 24 2 AAR40532 Aar40532 ID-Ala132
993 49 72.1 24 2 AAR40699 Aar40699 [Ser1351r
994 49 72.1 24 2 AAR40705 Aar40705 [Ser1361h
995 49 72.1 24 2 AAR40414 Aar40414 ID-Ala131
996 49 72.1 24 2 AAR40419 Aar40419 ID-Ala132
997 49 72.1 24 2 AAR40459 Aar40459 ID-Ala14
998 49 72.1 24 2 AAR40465 Aar40465 ID-Ala145
999 49 72.1 24 2 AAR40554 Aar40554 ID-Ala132
1000 49 72.1 24 2 AAR40420 Aar40420 ID-Ala132
```

ALIGNMENTS

```
RESULT 1
ABG98259 standard; peptide; 17 AA.
ID ABG98259;
XX
AC ABG98259;
XX
DT 08-JAN-2003 (first entry)
XX
DE Human C-type natriuretic peptide (CNP) variant #53.
XX
KW Human: natriuretic peptide; NP; endochondral ossification;
XX bone formation; cartilage; bone; signalling pathway; FGF;
XX fibroblast growth factor; cardiovascular homeostasis; diuresis;
XX natriuretic; vasodilation; atrial natriuretic peptide; ANP;
XX brain natriuretic peptide; BNP; C-type natriuretic peptide; CNP;
XX dendroaspis natriuretic peptide; DNP; NPR-A; NPR-B;
XX guanylyl cyclase domain; cGMP; neutral endopeptidase; NEP;
XX skeletal dysplasia; achondroplasia; osteopathic.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200274234-A2.
XX
PD 26-SEP-2002.
XX
PF 20-MAR-2002; 2002WO-IL000229.
XX
PR 20-MAR-2001; 2001IL-00142118.
XX
PR 20-MAR-2001; 2001US-0276939P.
XX
PA (PROC-) PROCHON BIOTECH LTD.
XX
PI Golemo M, Yavon A;
XX
DR WPI; 2002-750515/81.
XX
PT Pharmaceutical composition useful in the treatment of skeletal dysplasias
XX e.g. achondroplasia comprises at least one natriuretic peptide.
XX
PS Example 6; Page 23; 41pp. English.
```

```
XX The invention discloses a pharmaceutical composition comprising at least
CC one natriuretic peptide (NP), or its variant, and a carrier or excipient.
CC Endochondral ossification is a fundamental mechanism for bone formation,
CC whereby cartilage is replaced by bone. Endochondral ossification is the
CC result of the concerted action of several signalling pathways, most
CC notably the pathway triggered by the activation of the fibroblast growth
CC factor (FGF). Natriuretic peptides are also known for their role in
CC cardiovascular homeostasis, diuresis, natriuresis and vasodilation. Four
CC isoforms exist - atrial natriuretic peptide (ANP), brain natriuretic
CC peptide (BNP), C-type natriuretic peptide (CNP) and the dendroaspis
CC natriuretic peptide (DNP). NP's effect their biological role through two
CC receptors, NPR-A and NPR-B, having cytoplasmic guanylyl cyclase domains
CC which are activated upon ligand binding and lead to accumulation of
CC intracellular cGMP. They are cleaved by neutral endopeptidases (NEPs) and
CC inhibition of the NEPs increases the concentration of the NPs in the
CC circulation. The invention discloses compositions comprising NP secreting
CC cells and methods for treating skeletal dysplasias involving
CC transplanting or implanting the natriuretic peptide secreting cells. The
CC NP secreting cells are useful in the manufacture of a medicament for the
CC treatment of skeletal dysplasia (e.g. achondroplasia), for elongation of
CC abnormal bone and for increasing the size of bone growth plate in
CC abnormal bone (e.g. limb bone). The compositions induce bone elongation
CC in abnormal bone growth and enhance NP stabilisation in circulation. The
CC sequences presented in ABG98202-ABG98272 are the CNP peptide and
CC variants, with differing levels of activity, designed from it. The
CC degenerate peptide is presented in ABG98206
XX
```

SQ Sequence 17 AA;

Query Match 82.4%; Score 56; DB 5; Length 17;
Best Local Similarity 58.8%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
OY 1 CFGXXXDRIGXXSXXGC 17
   ||| ||| ||| |||
Db 1 CFGKLDRIGSWSALGC 17
```

```
RESULT 2
ABG98264 standard; peptide; 17 AA.
ID ABG98264;
XX
AC ABG98264;
XX
DT 08-JAN-2003 (first entry)
XX
DE Human C-type natriuretic peptide (CNP) variant #58.
XX
KW Human: natriuretic peptide; NP; endochondral ossification;
XX bone formation; cartilage; bone; signalling pathway; FGF;
XX fibroblast growth factor; cardiovascular homeostasis; diuresis;
XX natriuresis; vasodilation; atrial natriuretic peptide; ANP;
XX brain natriuretic peptide; BNP; C-type natriuretic peptide; CNP;
XX dendroaspis natriuretic peptide; DNP; NPR-A; NPR-B;
XX guanylyl cyclase domain; cGMP; neutral endopeptidase; NEP;
XX skeletal dysplasia; achondroplasia; osteopathic.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200274234-A2.
XX
PD 26-SEP-2002.
XX
PF 20-MAR-2002; 2002WO-IL000229.
XX
PR 20-MAR-2001; 2001IL-00142118.
XX
PR 20-MAR-2001; 2001US-0276939P.
XX
PA (PROC-) PROCHON BIOTECH LTD.
XX
PI Golemo M, Yavon A;
```

XX DR WPI: 2002-750515/81.
 XX XX
 PT Pharmaceutical composition useful in the treatment of skeletal dysplasias
 XX e.g. achondroplasia comprises at least one natriuretic peptide.
 XX XX
 PS Example 6; Page 23; 41pp; English.
 XX XX
 CC The invention discloses a pharmaceutical composition comprising at least
 CC one natriuretic peptide (NP), or its variant, and a carrier or excipient.
 CC Endochondral ossification is a fundamental mechanism for bone formation,
 CC whereby cartilage is replaced by bone. Endochondral ossification is the
 CC result of the concerted action of several signalling pathways, most
 CC notably the pathway triggered by the activation of the fibroblast growth
 CC factor (FGF). Natriuretic peptides are also known for their role in
 CC cardiovascular homeostasis, diuresis, natriuresis and vasodilatation. Four
 CC isoforms exist - atrial natriuretic peptide (ANP), brain natriuretic
 CC peptide (BNP), C-type natriuretic peptide (CNP) and the dendroaspis
 CC natriuretic peptide (DNP). NP's effect their biological role through two
 CC receptors, NPR-A and NPR-B, having cytoplasmic guanylyl cyclase domains
 CC which are activated upon ligand binding and lead to accumulation of
 CC intracellular cGMP. They are cleaved by neutral endopeptidases (NEPs) and
 CC inhibition of the NEPs increases the concentration of the NPs in the
 CC circulation. The invention discloses compositions comprising NP secreting
 CC cells and methods for treating skeletal dysplasias involving
 CC transplanting or implanting the natriuretic peptide secreting cells. The
 CC NP secreting cells are useful in the manufacture of a medicament for the
 CC treatment of skeletal dysplasia (e.g. achondroplasia), for elongation of
 CC abnormal bone and for increasing the size of bone growth plate in
 CC abnormal bone (e.g. limb bone). The compositions induce bone elongation
 CC in abnormal bone growth and enhance NP stabilisation in circulation. The
 CC sequences presented in ABG98202-ABG98272 are the CNP peptide and
 CC variants, with differing levels of activity, designed from it. The
 CC degenerate peptide is presented in ABG98206
 XX XX
 SQ Sequence 17 AA;
 Query Match 82.4%; Score 56; DB 5; Length 17;
 Best Local Similarity 58.8%; Pred. No. 0.00035;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CFGXXXXRIGXXXXXGC 17
 Db 1 CFGAKLDRIGMSGAGC 17
 RESULT 3
 ID ABG98241 standard; peptide: 17 AA.
 XX AC ABG98241;
 XX DT 08-JAN-2003 (first entry)
 XX DE Human C-type natriuretic peptide (CNP) variant #35.
 XX KW Human; natriuretic peptide; NP; endochondral ossification;
 KW bone formation; cartilage; bone; signalling pathway; FGF;
 KW fibroblast growth factor; cardiovascular homeostasis; diuresis;
 KW natriuresis; vasodilatation; atrial natriuretic peptide; ANP;
 KW brain natriuretic peptide; BNP; C-type natriuretic peptide; CNP;
 KW dendroaspis natriuretic peptide; DNP; NPR-A; NPR-B;
 KW guanylyl cyclase domain; cGMP; neutral endopeptidase; NEP;
 KW skeletal dysplasia; achondroplasia; osteopathic.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN WO200274234-A2.
 XX PD 26-SEP-2002.
 XX PF 20-MAR-2002; 2002WO-IL000229.

XX XX
 PR 20-MAR-2001; 2001IL-00142118.
 PR 20-MAR-2001; 2001US-0276939P.
 XX XX
 PA (PROC-) PROCHON BIOTECH LTD.
 XX XX
 PI Golembio M, Yayon A;
 XX XX
 DR WPI: 2002-750515/81.
 XX XX
 PT Pharmaceutical composition useful in the treatment of skeletal dysplasias
 PT e.g. achondroplasia comprises at least one natriuretic peptide.
 XX XX
 PS Example 6; Page 23; 41pp; English.
 XX XX
 CC The invention discloses a pharmaceutical composition comprising at least
 CC one natriuretic peptide (NP), or its variant, and a carrier or excipient.
 CC Endochondral ossification is a fundamental mechanism for bone formation,
 CC whereby cartilage is replaced by bone. Endochondral ossification is the
 CC result of the concerted action of several signalling pathways, most
 CC notably the pathway triggered by the activation of the fibroblast growth
 CC factor (FGF). Natriuretic peptides are also known for their role in
 CC cardiovascular homeostasis, diuresis, natriuresis and vasodilatation. Four
 CC isoforms exist - atrial natriuretic peptide (ANP), brain natriuretic
 CC peptide (BNP), C-type natriuretic peptide (CNP) and the dendroaspis
 CC natriuretic peptide (DNP). NP's effect their biological role through two
 CC receptors, NPR-A and NPR-B, having cytoplasmic guanylyl cyclase domains
 CC which are activated upon ligand binding and lead to accumulation of
 CC intracellular cGMP. They are cleaved by neutral endopeptidases (NEPs) and
 CC inhibition of the NEPs increases the concentration of the NPs in the
 CC circulation. The invention discloses compositions comprising NP secreting
 CC cells and methods for treating skeletal dysplasias involving
 CC transplanting or implanting the natriuretic peptide secreting cells. The
 CC NP secreting cells are useful in the manufacture of a medicament for the
 CC treatment of skeletal dysplasia (e.g. achondroplasia), for elongation of
 CC abnormal bone and for increasing the size of bone growth plate in
 CC abnormal bone (e.g. limb bone). The compositions induce bone elongation
 CC in abnormal bone growth and enhance NP stabilisation in circulation. The
 CC sequences presented in ABG98202-ABG98272 are the CNP peptide and
 CC variants, with differing levels of activity, designed from it. The
 CC degenerate peptide is presented in ABG98206
 XX XX
 SQ Sequence 17 AA;
 Query Match 82.4%; Score 56; DB 5; Length 17;
 Best Local Similarity 58.8%; Pred. No. 0.00035;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CFGXXXXRIGXXXXXGC 17
 Db 1 CFGAKLDRIGMSGAGC 17
 RESULT 4
 ID ABG98246 standard; peptide: 17 AA.
 XX AC ABG98246;
 XX DT 08-JAN-2003 (first entry)
 XX DE Human C-type natriuretic peptide (CNP) variant #40.
 XX KW Human; natriuretic peptide; NP; endochondral ossification;
 KW bone formation; cartilage; bone; signalling pathway; FGF;
 KW fibroblast growth factor; cardiovascular homeostasis; diuresis;
 KW natriuresis; vasodilatation; atrial natriuretic peptide; ANP;
 KW brain natriuretic peptide; BNP; C-type natriuretic peptide; CNP;
 KW dendroaspis natriuretic peptide; DNP; NPR-A; NPR-B;
 KW guanylyl cyclase domain; cGMP; neutral endopeptidase; NEP;
 KW skeletal dysplasia; achondroplasia; osteopathic.
 XX OS Homo sapiens.

OS	Synthetic.
XX	
PN	WO200274234-A2.
PD	
PP	26-SEP-2002.
PR	
PE	20-MAR-2002; 2002MO-IL0000229.
XX	
XX	20-MAR-2001; 2001IL-00142118.
PR	20-MAR-2001; 2001US-0276939P.
XX	
PA	(PROC-) PROCHON BIOTECH LTD.
XX	
P1	Golembo M., Yayon A;
XX	
DR	WPI; 2002-750515/81.
XX	
PT	Pharmaceutical composition useful in the treatment of skeletal dysplasias
PT	e.g. achondroplasia comprises at least one natriuretic peptide.
XX	
PS	Example 6; Page 23; 41pp; English.
CC	The invention discloses a pharmaceutical composition comprising at least
CC	one natriuretic peptide (NP), or its variant, and a carrier or excipient.
CC	Endochondral ossification is a fundamental mechanism for bone formation,
CC	whereby cartilage is replaced by bone. Endochondral ossification is the
CC	result of the concerted action of several signalling pathways, most
CC	notably the pathway triggered by the activation of the fibroblast growth
CC	factor (FGF). Natriuretic peptides are also known for their role in
CC	cardiovascular homeostasis, diuresis, natriuresis and vasodilatation. Four
CC	isoforms exist - atrial natriuretic peptide (ANP), brain natriuretic
CC	peptide (BNP), C-type natriuretic peptide (CNP) and the dendroaspis
CC	natriuretic peptide (DNP). NP's effect their biological role through two
CC	receptors, NPR-A and NPR-B, having cytoplasmic guanylyl cyclase domains
CC	which are activated upon ligand binding and lead to accumulation of
CC	intracellular cGMP. They are cleaved by neutral endopeptidases (NEPs) and
CC	inhibition of the NEPs increases the concentration of the NPs in the
CC	circulation. The invention discloses compositions comprising NP secreting
CC	cells and methods for treating skeletal dysplasias involving
CC	transplanting or implanting the natriuretic peptide secreting cells. The
CC	NP secreting cells are useful in the manufacture of a medicament for the
CC	treatment of skeletal dysplasia (e.g. achondroplasia), for elongation of
CC	abnormal bone and/or for increasing the size of bone growth plate in
CC	abnormal bone (e.g. limb bone). The compositions induce bone elongation
CC	in abnormal bone growth and enhance NP stabilisation in circulation. The
CC	sequences presented in ABG98202-ABG98272 are the CNP peptide and
CC	variants, with differing levels of activity, designed from it. The
CC	degenerate peptide is presented in ABG98206
XX	
SQ	Sequence 17 AA;
	Query Match 82.4%; Score 56; DB 5; Length 17;
	Best Local Similarity 58.8%; Pred. No. 0.00035;
	Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0
Oy	1 CFGXXXDRIGKXSSXGC 17
Db	1 CFGKLADRIGSMSGLC 17
RESULT 5	
ABG98269	ID ABG98269 standard; peptide; 17 AA.
AC	ABG98269;
XX	
DT	08-JAN-2003 (first entry)
XX	
DE	Human C-type natriuretic peptide (CNP) variant #63.
XX	
KW	Human; natriuretic peptide; NP; endochondral ossification;
KW	bone formation; cartilage; bone; signalling pathway; FGF;
KW	fibroblast growth factor; cardiovascular homeostasis; diuresis;

KW	natriuretic; vasodilation; atrial natriuretic peptide; ANP;	
KW	brain natriuretic peptide; BNP, C-type natriuretic peptide; CNP;	
KW	dendroaspis natriuretic peptide; DNP; NPR-A; NPR-B;	
KW	guanylyl cyclase domain; CGMP; neutral endopeptidase; NEP;	
XX	skeletal dysplasia; achondroplasia; osteopathic.	
OS	Homo sapiens.	
OS	Synthetic.	
XX	WO200274234-A2.	
XX	26-SEP-2002.	
XX		
XX	20-MAR-2002; 2002WO-IL000229.	
XX		
XX	20-MAR-2001; 2001IL-00142118.	
XX	20-MAR-2001; 2001US-0276939P.	
XX		
XX	(PROC-) PROCHON BIOTECH LTD.	
XX		
XX	Golembu M, Yayon A;	
XX	WPI; 2002-750515/81.	
XX		
XX	Pharmaceutical composition useful in the treatment of skeletal dysplasias	
XX	e.g. achondroplasia comprises at least one natriuretic peptide.	
XX		
XX	Example 6; Page 23; 41pp; English.	
XX		
XX	The invention discloses a pharmaceutical composition comprising at least	
XX	one natriuretic peptide (NP), or its variant, and a carrier or excipient.	
XX	Endochondral ossification is a fundamental mechanism for bone formation,	
XX	whereby cartilage is replaced by bone. Endochondral ossification is the	
XX	result of the concerted action of several signalling pathways, most	
XX	notably the pathway triggered by the activation of the fibroblast growth	
XX	factor (FGF). Natriuretic peptides are also known for their role in	
XX	cardiovascular homeostasis, diuresis, natriuresis and vasodilation. Four	
XX	isoforms exist - atrial natriuretic peptide (ANP), brain natriuretic	
XX	peptide (BNP), C-type natriuretic peptide (CNP) and the dendroaspis	
XX	natriuretic peptide (DNP). NP's effect their biological role through two	
XX	receptors, NPR-A and NPR-B, having cytoplasmic guanylyl cyclase domains	
XX	which are activated upon ligand binding and lead to accumulation of	
XX	intracellular cGMP. They are cleaved by neutral endopeptidases (NEPs) and	
XX	inhibition of the NEPs increases the concentration of the NPs in the	
XX	circulation. The invention discloses compositions comprising NP secreting	
XX	cells and methods for treating skeletal dysplasias involving	
XX	transplanting or implanting the natriuretic peptide secreting cells. The	
XX	NP secreting cells are useful in the manufacture of a medicament for the	
XX	treatment of skeletal dysplasia (e.g. achondroplasia), for elongation of	
XX	abnormal bone and for increasing the size of bone growth plate in	
XX	abnormal bone (e.g. limb bone). The compositions induce bone elongation	
XX	in abnormal bone growth and enhance NP stabilisation in circulation. The	
XX	sequences presented in ABG98202-ABG98272 are the CNP peptide and	
XX	variants, with differing levels of activity, designed from it. The	
XX	degenerate peptide is presented in ABG98206	
XX		
XX	Sequence 17 AA;	
XX		
XX	Query Match 82.4%; Score 56; DB 5; Length 17;	
XX	Best Local Similarity 58.8%; Pred. NO. 0.00035;	
XX	Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0	
XX		
XX	1 CFGKXXDRIGKXXSGC 17	
XX		
XX	1 CFGKXDRIGSSSGLG 17	
XX		
XX	RESULT 6	
XX	ABG98211	
XX	ID ABG98211 standard; peptide; 17 AA.	
XX	ABG98211;	
XX		

DT 08-JAN-2003 (first entry)
 XX
 DE Human C-type natriuretic peptide (CNP) variant #5.
 XX
 KW Human; natriuretic peptide; NP; endochondral ossification;
 KW bone formation; cartilage; bone; signaling pathway; FGF;
 KW fibroblast growth factor; cardiovascular homeostasis; diuresis;
 KW natriuresis; vasodilation; atrial natriuretic peptide; ANP;
 KW brain natriuretic peptide; BNP; C-type natriuretic peptide; CNP;
 KW dendroaapla natriuretic peptide; DNP; NPR-A; NPR-B;
 KW guanylyl cyclase domain; cGMP; neutral endopeptidase; NEP;
 KW skeletal dysplasia; achondroplasia; osteopathic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN WO200274234-A2.
 XX
 PD 26-SEP-2002.
 XX
 PF 20-MAR-2002; 2002WO-IL000229.
 XX
 PR 20-MAR-2001; 2001IL-00142118.
 PR 20-MAR-2001; 2001US-0276939P.
 XX
 PA (PROC-) PROCHON BIOTECH LTD.
 XX
 PI Golembio M, Yaron A;
 XX
 DR WPI; 2002-750515/81.
 XX
 PT Pharmaceutical composition useful in the treatment of skeletal dysplasias
 PT e.g. achondroplasia comprises at least one natriuretic peptide.
 XX
 PS Example 6; Page 22; 41pp; English.
 XX
 SQ The invention discloses a pharmaceutical composition comprising at least
 CC one natriuretic peptide (NP), or its variant, and a carrier or excipient.
 CC Endochondral ossification is a fundamental mechanism for bone formation,
 CC whereby cartilage is replaced by bone. Endochondral ossification is the
 CC result of the concerted action of several signalling pathways, most
 CC notably the pathway triggered by the activation of the fibroblast growth
 CC factor (FGF). Natriuretic peptides are also known for their role in
 CC cardiovascular homeostasis, diuresis, natriuresis and vasodilation. Four
 CC isoforms exist - atrial natriuretic peptide (ANP), brain natriuretic
 CC peptide (BNP), C-type natriuretic peptide (CNP) and the dendroaapis
 CC natriuretic peptide (DNP). NP's effect their biological role through two
 CC receptors, NPR-A and NPR-B, having cytoplasmic guanylyl cyclase domains
 CC which are activated upon ligand binding and lead to accumulation of
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 CC circulation. The invention discloses compositions comprising NP secreting
 CC cells and methods for treating skeletal dysplasias involving
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 CC NP secreting cells are useful in the manufacture of a medicament for the
 CC treatment of skeletal dysplasia (e.g. achondroplasia), for elongation of
 CC abnormal bone and for increasing the size of bone growth plate in
 CC abnormal bone (e.g. limb bone). The compositions induce bone elongation
 CC in abnormal bone growth and enhance NP stabilisation in circulation. The
 CC sequences presented in ABG98202-ABG98272 are the CNP peptide and
 CC variants, with differing levels of activity, designed from it. The
 CC degenerate peptide is presented in ABG98206
 XX
 SQ Sequence 17 AA;
 Query Match 82.4%; Score 56; DB 5; Length 17;
 Best Local Similarity 58.8%; Pred. No. 0.00035;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGLKDRIGSASGLGC 17
 DB 1 CFGLKDRIGSASGLGC 17

RESULT 7
 AAR40630
 ID AAR40630 standard; protein; 18 AA.
 XX
 AC AAR40630;
 XX
 DT 25-MAR-2003 (revised)
 DT 14-SEP-1993 (first entry)
 XX
 DE [Arg129] [D-Ala143] hANVP(130-146)-NH2.
 XX
 KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 KW
 XX
 OS Synthetic.
 OS
 PN US5212286-A.
 XX
 PD 18-MAY-1993.
 XX
 PF 05-JUN-1986; 86US-00870795.
 XX
 PR 19-APR-1984; 84US-00602117.
 PR 01-JUN-1984; 84US-00616488.
 PR 08-MAY-1985; 85US-0076030.
 XX
 PA (SCIO-) SCIOS NOVA INC.
 XX
 PI Lewicki JA, Scarborough RW;
 XX
 DR WPI; 1993-175525/21.
 XX
 PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
 PT in mammals.
 XX
 PS Disclosure; Col 48; 45pp; English.
 XX
 CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
 CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
 CC fluid volume and blood pressure in host organisms. These ANVP fragments
 CC may be produced by solid-phase techniques. See also AAR36937-78. (updated
 CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
 CC PR field.)
 CC
 XX
 SQ Sequence 18 AA;
 Query Match 82.4%; Score 56; DB 2; Length 18;
 Best Local Similarity 58.8%; Pred. No. 0.00036;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGLKDRIGSASGLGC 17
 DB 2 CFGLKDRIGSASGLGC 18
 RESULT 8
 AAR40624
 ID AAR40624 standard; protein; 18 AA.
 XX
 AC AAR40624;
 XX
 DT 25-MAR-2003 (revised)
 DT 14-SEP-1993 (first entry)
 XX
 DE [Arg129] [D-Ala133] hANVP(130-146)-NH2.

```

XX Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
PH Disulfide-bond 2. .18
FT Misc-difference 5
FT /note= "D form residue"
FT Modified-site 18
FT /note= "Amidated C terminal"
XX
XX US5212286-A.
XX
XX 18-MAY-1993.
XX
XX 05-JUN-1986; 86US-00870795.
XX
XX 19-APR-1984; 84US-00602117.
XX 01-JUN-1984; 84US-00616488.
XX 08-MAY-1985; 85US-00766030.
XX
XX (SCIO-) SCIOS NOVA INC.
XX
XX Lewicki JA, Scarborough RM;
XX
XX WPI; 1993-175525/21.
XX
XX New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
XX in mammals.
XX
XX PS Disclosure; Col 47; 45pp; English.
XX
XX CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
XX CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
XX CC fluid volume and blood pressure in host organisms. These ANVP fragments
XX CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
XX CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
XX CC PR field.)
XX
XX SQ Sequence 18 AA;

Query Match 82.4%; Score 56; DB 2; Length 18;
Best Local Similarity 58.8%; Pred. No. 0.00036;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXXXXGC 17
   ||| ||| ||| |||
Db 2 CFGARMDRIGAQSGALGC 18

RESULT 9
AAR40627
ID AAR40627 standard; protein; 18 AA.
XX
XX AAR40627;
XX
XX 25-MAR-2003 (revised)
XX 14-SEP-1993 (first entry)
XX
XX [Arg128] [D-Ala142] rANVP(129-145)-NH2.
XX Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
XX regulation; fluid volume; blood pressure.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX FH Disulfide-bond 2. .18
XX FT Misc-difference 15
XX FT /note= "D form residue"
XX FT Modified-site 18

```

```

FT /note= "Amidated C terminal"
XX
XX US5212286-A.
XX
XX 18-MAY-1993.
XX
XX 05-JUN-1986; 86US-00870795.
XX
XX 19-APR-1984; 84US-00602117.
XX 01-JUN-1984; 84US-00616488.
XX 08-MAY-1985; 85US-00766030.
XX
XX (SCIO-) SCIOS NOVA INC.
XX
XX Lewicki JA, Scarborough RM;
XX
XX WPI; 1993-175525/21.
XX
XX New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
XX in mammals.
XX
XX PS Disclosure; Col 47; 45pp; English.
XX
XX CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
XX CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
XX CC fluid volume and blood pressure in host organisms. These ANVP fragments
XX CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
XX CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
XX CC PR field.)
XX
XX SQ Sequence 18 AA;

Query Match 82.4%; Score 56; DB 2; Length 18;
Best Local Similarity 58.8%; Pred. No. 0.00036;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXXXXGC 17
   ||| ||| ||| |||
Db 2 CFGGRIDRIGAQSGALGC 18

RESULT 10
AAR40621
ID AAR40621 standard; protein; 18 AA.
XX
XX AAR40621;
XX
XX 25-MAR-2003 (revised)
XX 14-SEP-1993 (first entry)
XX
XX [Arg128] [D-Ala132] rANVP(129-145)-NH2.
XX Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
XX regulation; fluid volume; blood pressure.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX FH Disulfide-bond 2. .18
XX FT Misc-difference 5
XX FT /note= "D form residue"
XX FT Modified-site 18
XX FT /note= "Amidated C terminal"
XX
XX US5212286-A.
XX
XX 18-MAY-1993.
XX
XX 05-JUN-1986; 86US-00870795.
XX
XX 19-APR-1984; 84US-00602117.
XX 01-JUN-1984; 84US-00616488.
XX 08-MAY-1985; 85US-00766030.

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XX (SCIO-) SCIOS NOVA INC.
XX PA
XX PI Lewicki JA, Scarborough RM;
XX DR WPI; 1993-175525/21.
XX PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
XX in mammals.
XX PS Disclosure; Col 47; 45pp; English.
CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX SQ Sequence 18 AA;
Query Match 82.4%; Score 56; DB 2; Length 18;
Best Local Similarity 58.8%; Pred. No. 0.0036;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY 1 CFCGXXDRIGXXSXXGC 17
    ||| ||| |||
    2 CFCARIDRIGAGSGLGC 18
Db
RESULT 11
AAR40455
ID AAR40455 standard; protein; 20 AA.
XX AC AAR40455;
XX DT 25-MAR-2003 (revised)
XX DT 14-SEP-1993 (first entry)
XX DE [D-A1a143]RANVP(127-146)-NH2.
XX KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
XX regulation; fluid volume; blood pressure.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Disulfide-bond 4..20
XX FT Misc-difference 17
XX FT /note= "D-form residue"
XX FT Modified-site 20
XX FT /note= "Amidated C-terminal"
XX PN US5212286-A.
XX PD 18-MAY-1993.
XX PF 05-JUN-1986; 86US-00870795.
XX PR 19-APR-1984; 84US-00602117.
XX PR 01-JUN-1984; 84US-00616488.
XX PR 08-MAY-1985; 85US-00766030.
XX PA (SCIO-) SCIOS NOVA INC.
XX PI Lewicki JA, Scarborough RM;
XX DR WPI; 1993-175525/21.
XX PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
XX in mammals.
XX PS Disclosure; Col 34; 45pp; English.

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XX The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
XX peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
XX fluid volume and blood pressure in host organisms. These ANVP fragments
XX may be produced by solid-phase techniques. See also AAR36937-78. (Updated
XX on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
XX PR field.)
XX SQ Sequence 20 AA;
Query Match 82.4%; Score 56; DB 2; Length 20;
Best Local Similarity 58.8%; Pred. No. 0.0004;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY 1 CFCGXXDRIGXXSXXGC 17
    ||| ||| |||
    4 CFCGRMDRIGAGSALGC 20
Db
RESULT 12
AAR40449
ID AAR40449 standard; protein; 20 AA.
XX AC AAR40449;
XX DT 25-MAR-2003 (revised)
XX DT 14-SEP-1993 (first entry)
XX DE [D-A1a142]RANVP(126-145)-NH2.
XX KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
XX regulation; fluid volume; blood pressure.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Disulfide-bond 4..20
XX FT Misc-difference 17
XX FT /note= "D-form residue"
XX FT Modified-site 20
XX FT /note= "Amidated C-terminal"
XX PN US5212286-A.
XX PD 18-MAY-1993.
XX PF 05-JUN-1986; 86US-00870795.
XX PR 19-APR-1984; 84US-00602117.
XX PR 01-JUN-1984; 84US-00616488.
XX PR 08-MAY-1985; 85US-00766030.
XX PA (SCIO-) SCIOS NOVA INC.
XX PI Lewicki JA, Scarborough RM;
XX DR WPI; 1993-175525/21.
XX PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
XX in mammals.
XX PS Disclosure; Col 33; 45pp; English.
CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX SQ Sequence 20 AA;
Query Match 82.4%; Score 56; DB 2; Length 20;

```

Best Local Similarity 58.8%; Pred. No. 0.0004; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXXXXGC 17
 ||| ||| ||| |||
 DB 4 CFGGRIDRIGAGSALGC 20

RESULT 13

AA040434
 ID AAR40434 standard; protein; 20 AA.

AC AAR40434;

DT 25-MAR-2003 (revised)
 DT 14-SEP-1993 (first entry)

DE [D-ALA133]ANVP (127-146) -NH2.

KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.

OS Synthetic.

PH Key Location/Qualifiers

FT Disulfide-bond 4. .20

FT Misc-difference 7 /note= "D-form residue"

FT Modified-site 20 /note= "Amidated C-terminal"

FT US5212286-A.

PN 18-MAY-1993.

PD 05-JUN-1986; 86US-00870795.

PF 19-APR-1984; 84US-00602117.

PR 01-JUN-1984; 84US-00616488.

PR 08-MAY-1985; 85US-00766030.

XX (SCIO-) SCIOS NOVA INC.

PI Lewicki JA, Scarborough RM;

XX WPI; 1993-175525/21.

DR New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator

PT in mammals.

XX Disclosure; Col 32; 45pp; English.

PS The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator

CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of

CC fluid volume and blood pressure in host organisms. These ANVP fragments

CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated

CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct

CC PR field.)

XX Sequence 20 AA;

Query Match 82.4%; Score 56; DB 2; Length 20;

Best Local Similarity 58.8%; Pred. No. 0.0004;

Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXXXXGC 17
 ||| ||| ||| |||
 DB 4 CFGARMDRIGAGSALGC 20

RESULT 14

AA040454
 ID AAR40454 standard; protein; 20 AA.

XX AAR40454;

DT 25-MAR-2003 (revised)

DT 14-SEP-1993 (first entry)

DE [D-ALA143]ANVP (127-149) -NH2.

KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;

OS Synthetic.

PH Key Location/Qualifiers

FT Disulfide-bond 4. .20

FT Misc-difference 17 /note= "D-form residue"

FT Modified-site 20 /note= "Amidated C-terminal"

FT US5212286-A.

PN 18-MAY-1993.

PD 05-JUN-1986; 86US-00870795.

PF 19-APR-1984; 84US-00602117.

PR 01-JUN-1984; 84US-00616488.

PR 08-MAY-1985; 85US-00766030.

XX (SCIO-) SCIOS NOVA INC.

PI Lewicki JA, Scarborough RM;

XX WPI; 1993-175525/21.

DR New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator

PT in mammals.

XX Disclosure; Col 33; 45pp; English.

CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator

CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of

CC fluid volume and blood pressure in host organisms. These ANVP fragments

CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated

CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct

CC PR field.)

XX Sequence 20 AA;

Query Match 82.4%; Score 56; DB 2; Length 20;

Best Local Similarity 58.8%; Pred. No. 0.0004;

Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXXXXGC 17
 ||| ||| ||| |||
 DB 4 CFGGRMDRIGAGSALGC 20

RESULT 15

AA040428
 ID AAR40428 standard; protein; 20 AA.

AC AAR40428;

DT 25-MAR-2003 (revised)

DT 14-SEP-1993 (first entry)

DE [D-ALA132]ANVP (126-145) -NH2.

KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;

KW regulation; fluid volume; blood pressure.

OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Disulfide-bond 4. 20
 FT Misc-difference 7
 FT Modified-site /note= "D-form residue"
 FT /note= "Amidated C-terminal"
 XX
 PN US5212286-A.
 XX
 PD 18-MAY-1993.
 XX
 PF 05-JUN-1986; 86US-00870795.
 XX
 PR 19-APR-1984; 84US-00602117.
 PR 01-JUN-1984; 84US-00616488.
 PR 08-MAY-1985; 85US-00766030.
 XX
 PA (SCIO-) SCIOS NOVA INC.
 XX
 PI Lewicki JA, Scarborough RM;
 XX
 DR WPI; 1993-175525/21.
 XX
 PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
 PT in mammals.
 XX
 PS Disclosure; Col 31; 45pp; English.
 XX
 CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
 CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
 CC fluid volume and blood pressure in host organisms. These ANVP fragments
 CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
 CC on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct
 CC PR field.)
 CC
 XX
 SQ Sequence 20 AA;
 Query Match 82.4%; Score 56; DB 2; Length 20;
 Best Local Similarity 58.8%; Pred. No. 0.0004;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CFGXXXXRIGXXSXXGC 17
 Db 4 CFGARIDRIGAGSLGC 20
 RESULT 16
 AAB91293
 ID AAB91293 standard; peptide; 20 AA.
 XX
 AC AAB91293;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Atrial-natriuretic peptide (ANP) SEQ ID NO:469.
 XX
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidy; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-US013576.
 XX
 PR 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.

PR 15-OCT-1999; 99US-0159783P.
 XX
 PA (CONU-) CONUICHEM INC.
 XX
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX
 DR WPI; 2001-112059/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX
 PS Disclosure; Page 352; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (II) and a
 CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 20 AA;
 Query Match 82.4%; Score 56; DB 4; Length 20;
 Best Local Similarity 58.8%; Pred. No. 0.0004;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CFGXXXXRIGXXSXXGC 17
 Db 1 CFGSRIDRIGAGSGMG 17
 RESULT 17
 ABB05585
 ID ABB05585 standard; peptide; 20 AA.
 XX
 AC ABB05585;
 XX
 DT 22-APR-2002 (first entry)
 XX
 DE Dithiol peptide #13.
 XX
 KW Dithiol; disulfide bond; chemical reagent; sulphydryl group; SH group;
 KW trans-(Pt(ethylenediamine)2Cl2)2+.
 XX
 OS Synthetic.
 OS
 PH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "acetylated"
 FT Modified-site 4
 FT /note= "amidated"
 XX
 PN WO200192466-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 16-MAY-2001; 2001WO-US015923.
 XX
 PR 26-MAY-2000; 2000US-00579883.
 XX
 PA (REGC) UNIV CALIFORNIA.

PI Rabenstein DA, Shi T;
 XX
 DR WPI; 2002-114335/15.
 XX
 PT Forming an intramolecular disulfide bond in a peptide, comprises
 PT connecting a peptide comprising at least two sulfhydryl groups with an
 PT oxidizing agent that forms disulfide linkages in peptides.
 XX
 PS Example 1; Page 15; 40pp; English.
 XX
 CC The present invention describes a method of forming an intramolecular
 CC disulfide bond in a peptide, comprising contacting a peptide comprising
 CC at least two sulfhydryl (SH) groups with a compound (trans-
 CC (P-ethylenediamine)2C12/12+) (I). Also describes are: (1) a solution (II)
 CC comprising a peptide which comprises at least two sulfur groups, and (1);
 CC (2) a peptide synthesizer (III) for the synthesis of a peptide having an
 CC intramolecular disulfide linkage, comprises a number of vials containing
 CC amino acids derivatised for chemical peptide synthesis, where at least
 CC one of the vials comprises an amino acid that, when fully deprotected,
 CC bears a SH group, and a vial comprising (I); (3) chemically synthesising
 CC a peptide comprising a disulfide linkage, involving chemically coupling a
 CC number of amino acids to form a peptide comprising at least two SH
 CC groups, and contacting the peptide with (I); and (4) a kit for forming an
 CC intramolecular disulfide bond in a peptide, comprises a container
 CC containing (I). The method can be used for forming an intramolecular
 CC disulfide bond in a peptide. (II) is useful as a positive control when
 CC evaluating the efficacy of particular reagent species, and as a sample
 CC solution when optimising a purification protocol to clean up or to
 CC isolate the desired reaction product (e.g., when optimising a high
 CC pressure liquid chromatography (HPLC) protocol or evaluating a particular
 CC chromatography column). The present sequence represents a dichloro peptide
 CC which is used in an example from the present invention
 XX
 SQ Sequence 20 AA;
 XX
 Query Match 82.4%; Score 56; DB 5; Length 20;
 Best Local Similarity 58.8%; Pred. No. 0.0004; 7; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CFGXXXDRIGXXSXXGC 17
 DB 1 CFGSRIDRIGAGSGMGC 17
 XX
 RESULT 18
 AAR03304
 ID AAR03304 standard; protein; 21 AA.
 XX
 AC AAR03304;
 XX
 DT 24-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 15-AUG-1990 (first entry)
 XX
 DE FANP-21 frog atrial natriuretic peptide.
 XX
 KW Atrial natriuretic peptide; FANP-21; diuretic; hypertensive.
 XX
 OS Rana catesbeiana.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..17
 XX
 PN JP02025500-A.
 XX
 PD 26-JAN-1990.
 XX
 PF 14-JUL-1988; 88JP-00173740.
 XX
 PR 14-JUL-1988; 88JP-00173740.
 XX
 PA (MATS/) MATSUO T.
 XX

DR WPI; 1990-071805/10.
 XX
 PT New peptide with physiological activity - obt'd. from heart of frog, has
 PT diuretic and antihypertensive properties.
 XX
 PS Claim 1; Fig 3; 8pp; Japanese.
 XX
 CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 21 AA;
 XX
 Query Match 82.4%; Score 56; DB 2; Length 21;
 Best Local Similarity 58.8%; Pred. No. 0.00042; 7; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CFGXXXDRIGXXSXXGC 17
 DB 1 CFGSRIDRIGAGSGMGC 17
 XX
 RESULT 19
 AAR40629
 ID AAR40629 standard; protein; 21 AA.
 XX
 AC AAR40629;
 XX
 DT 25-MAR-2003 (revised)
 DT 14-SEP-1993 (first entry)
 XX
 DE [Arg129] [D-Ala143] hANVP (130-149) -NH2.
 XX
 KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 2..18
 FT Misc-difference 15
 FT Modified-site 21
 FT FT /note= "D form residue"
 FT FT /note= "Amidated C terminal"
 XX
 PN US5212286-A.
 XX
 PD 18-MAY-1993.
 XX
 PF 05-JUN-1986; 86US-00870795.
 XX
 PR 19-APR-1984; 84US-00602117.
 PR 01-JUN-1984; 84US-00616488.
 PR 08-MAY-1985; 85US-00766030.
 XX
 PA (SCIO-) SCIOS NOVA INC.
 XX
 PI Lewicki JA, Scarborough RM;
 XX
 DR WPI; 1993-175525/21.
 XX
 PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
 PT in mammals.
 XX
 PS Disclosure; Col 48; 45pp; English.
 XX
 CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
 CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
 CC fluid volume and blood pressure in host organisms. These ANVP fragments
 CC may be produced by solid-phase techniques. See also AAR36337-78. (Updated
 CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
 CC PR field.)
 XX
 SQ Sequence 21 AA;
 XX

Query Match 82.4%; Score 56; DB 2; Length 21;
 Best Local Similarity 58.8%; Pred. No. 0.00042;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXXRIGXXSXXGC 17
 ||| ||| ||| ||| |||
 DB 2 CFGGRMDRIGAGSALGC 18

RESULT 20

AAK40620
 ID AAK40620 standard; protein; 21 AA.

XX AAK40620;

DT 25-MAR-2003 (revised)
 DT 14-SEP-1993 (first entry)

DE [Arg128] [D-Ala132] rANVP(129-148)-NH2.

XX Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.

XX Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 2..18

FT Misc-difference 5 /note= "D form residue"

FT Modified-site 21 /note= "Amidated C terminal"

XX US5212286-A.

XX 18-MAY-1993.

XX 05-JUN-1986; 86US-00870795.

XX 19-APR-1984; 84US-00602117.

XX 01-JUN-1984; 84US-00616488.

XX 08-MAY-1985; 85US-00766030.

XX (SCIO-) SCIOS NOVA INC.

XX PI Lewicki JA, Scarborough RM;

XX WPI; 1993-175525/21.

XX PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator

XX in mammals.

XX Disclosure; Col 47; 45pp; English.

XX The sequences given in AAK40387-748 are atrial natriuretic/ vasodilator
 CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
 CC fluid volume and blood pressure in host organisms. These ANVP fragments
 CC may be produced by solid-phase techniques. See also AAK36937-78. (Updated
 CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
 CC PR field.)

XX Sequence 21 AA;

Query Match 82.4%; Score 56; DB 2; Length 21;
 Best Local Similarity 58.8%; Pred. No. 0.00042;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXXRIGXXSXXGC 17
 ||| ||| ||| ||| |||
 DB 2 CFGARIDRIGAGSGLGC 18

RESULT 21

AAK40623
 ID AAK40623 standard; protein; 21 AA.

XX AAK40623;

DT 25-MAR-2003 (revised)
 DT 14-SEP-1993 (first entry)

DE [Arg129] [D-Ala133] hANVP(130-149)-NH2.

XX Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.

XX Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 2..18

FT Misc-difference 5 /note= "D form residue"

FT Modified-site 21 /note= "Amidated C terminal"

XX US5212286-A.

XX 18-MAY-1993.

XX 05-JUN-1986; 86US-00870795.

XX 19-APR-1984; 84US-00602117.

XX 01-JUN-1984; 84US-00616488.

XX 08-MAY-1985; 85US-00766030.

XX (SCIO-) SCIOS NOVA INC.

XX PI Lewicki JA, Scarborough RM;

XX WPI; 1993-175525/21.

XX PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator

XX in mammals.

XX Disclosure; Col 47; 45pp; English.

XX The sequences given in AAK40387-748 are atrial natriuretic/ vasodilator
 CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
 CC fluid volume and blood pressure in host organisms. These ANVP fragments
 CC may be produced by solid-phase techniques. See also AAK36937-78. (Updated
 CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
 CC PR field.)

XX Sequence 21 AA;

Query Match 82.4%; Score 56; DB 2; Length 21;
 Best Local Similarity 58.8%; Pred. No. 0.00042;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFGXXXXRIGXXSXXGC 17
 ||| ||| ||| ||| |||
 DB 2 CFGARMDRIGAGSGLGC 18

RESULT 22

AAK40626
 ID AAK40626 standard; protein; 21 AA.

XX AAK40626;

DT 25-MAR-2003 (revised)
 DT 14-SEP-1993 (first entry)

DE [Arg128] [D-Ala142] rANVP(129-148)-NH2.

XX Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;

```

KW regulation; fluid volume; blood pressure.
XX Synthetic.
OS
XX Key Location/Qualifiers
FH Disulfide-bond 2..18
FT Misc-difference 15
FT /note= "D form residue"
FT Modified-site 21
FT /note= "Amidated C terminal"
XX
XX US5212286-A.
XX
XX 18-MAY-1993.
XX
XX 05-JUN-1986; 86US-00870795.
XX
XX 19-APR-1984; 84US-00602117.
XX 01-JUN-1984; 84US-00616488.
XX 08-MAY-1985; 85US-00766030.
XX
XX (SCTO-) SCTOS NOVA INC.
XX
XX PA
XX PI Lewicki JA, Scarborough RM;
XX DR WPI; 1993-175525/21.
XX
XX PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
XX PT in mammals.
XX
XX PS Disclosure; Col 47; 45pp; English.
XX
XX CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
XX CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
XX CC fluid volume and blood pressure in host organisms. These ANVP fragments
XX CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
XX CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
XX CC PR field.)
XX
XX SQ Sequence 21 AA;
XX
XX Query Match 82.4%; Score 56; DB 2; Length 21;
XX Best Local Similarity 58.8%; Pred. No. 0.00042;
XX Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
XX
XX QY 1 CFGXXXXRIGXXSXXGC 17
XX Db 2 CFGGRIDRIGAGSALGC 18
XX
XX RESULT 23
XX AAB91294
XX ID AAB91294 standard; peptide; 21 AA.
XX
XX AC AAB91294;
XX
XX DT 22-JUN-2001 (first entry)
XX
XX DE Atrial-natriuretic peptide (ANP) SEQ ID NO:470.
XX
XX OS Protection; endogenous therapeutic peptide; peptidase; conjugation;
XX OS blood component; modification; succinimidy1, maleimido group; amino;
XX OS hydroxy1; thiol; hormone; growth factor; neurotransmitter.
XX OS Synthetic.
XX OS Homo sapiens.
XX OS
XX PN WO200069900-A2.
XX
XX PD 23-NOV-2000.
XX
XX PF 17-MAY-2000; 2000WO-US013576.
XX

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PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
XX (CONJ-) CONJUCHEM INC.
XX
XX PA
XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX DR WPI; 2001-112059/12.
XX
XX PT Modifying and attaching therapeutic peptides to albumin prevents
XX PT peptidase degradation, useful for increasing length of in vivo activity.
XX
XX PS Disclosure; Page 352; 733pp; English.
XX
XX CC The present invention describes a modified therapeutic peptide (I)
XX CC comprising a therapeutically active amino acid region (iii) and a
XX CC reactive group (ii) (e.g. succinimidy1 and maleimido groups) attached to
XX CC a less therapeutically active amino acid region (iv), which covalently
XX CC bonds with amino/hydroxy1/thiol groups on blood components to form a
XX CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
XX CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
XX CC factors and neurotransmitters, to protect them from peptidase activity in
XX CC vivo for the treatment of various disorders. Endogenous therapeutic
XX CC peptides are not suitable as drug candidates as they require frequent
XX CC administration due to rapid degradation by peptidases in the body.
XX CC Modifying and attaching therapeutic peptides to albumin prevents or
XX CC reduces the action of peptidases to increase length of activity (half
XX CC life) and specificity as bonding to large molecules decreases
XX CC intracellular uptake and interference with physiological processes.
XX CC AAB90829 to AAB92441 represent peptides which can be used in the
XX CC exemplification of the present invention
XX
XX SQ Sequence 21 AA;
XX
XX Query Match 82.4%; Score 56; DB 4; Length 21;
XX Best Local Similarity 58.8%; Pred. No. 0.00042;
XX Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
XX
XX QY 1 CFGXXXXRIGXXSXXGC 17
XX Db 1 CFGGRIDRIGAGSGWGC 17
XX
XX RESULT 24
XX AAR40448
XX ID AAR40448 standard; protein; 23 AA.
XX
XX AC AAR40448;
XX
XX DT 25-MAR-2003 (revised)
XX DT 14-SEP-1993 (first entry)
XX
XX DE [D-Ala142]ANVP(126-148)-NH2.
XX
XX KM Human, pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
XX KM regulation; fluid volume; blood pressure.
XX
XX OS Synthetic.
XX OS
XX FH Key Location/Qualifiers
XX FT Disulfide-bond 4..20
XX FT Misc-difference 17
XX FT /note= "D-form residue"
XX FT Modified-site 23
XX FT /note= "Amidated C-terminal"
XX
XX PN US5212286-A.
XX
XX PD 18-MAY-1993.
XX
XX PF 05-JUN-1986; 86US-00870795.
XX

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PR 19-APR-1984; 84US-00602117.
 PR 01-JUN-1984; 84US-00616488.
 PR 08-MAY-1985; 85US-00766030.
 XX
 PA (SCIO-) SCTOS NOVA INC.
 XX
 PI Lewicki JA, Scarborough RM;
 XX
 DR WPI, 1993-175525/21.
 XX
 PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
 XX in mammals.
 XX
 PS Disclosure; Col 33; 45pp; English.
 XX
 CC The sequences given in AAR40387-748 are atrial natriuretic/vasodilator
 CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
 CC fluid volume and blood pressure in host organisms. These ANVP fragments
 CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
 CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
 CC PR field.)
 CC
 XX
 SQ Sequence 23 AA;
 XX
 Query Match 82.4%; Score 56; DB 2; Length 23;
 Best Local Similarity 58.8%; Pred. No. 0.00046;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 OY 1 CFGXXXDRIGXXSXGC 17
 ||| ||| |||
 DB 4 CFGGRIDRIGAGSALGC 20
 XX
 RESULT 25
 AAR36975
 ID AAR36975 standard; protein; 23 AA.
 XX
 AC AAR36975;
 XX
 DT 25-MAR-2003 (revised)
 DT 14-SEP-1993 (first entry)
 XX
 DE ANVP #39.
 XX
 KM Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 KM regulation; fluid volume; blood pressure.
 XX
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Disulfide-bond 2..18
 FT Misc-difference 5 /note= "D-form residue"
 XX
 PN US5212286-A.
 XX
 PD 18-MAY-1993.
 XX
 PF 05-JUN-1986; 86US-00870795.
 XX
 PR 19-APR-1984; 84US-00602117.
 PR 01-JUN-1984; 84US-00616488.
 PR 08-MAY-1985; 85US-00766030.
 XX
 PA (SCIO-) SCTOS NOVA INC.
 XX
 PI Lewicki JA, Scarborough RM;
 XX
 DR WPI, 1993-175525/21.
 XX
 PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
 XX in mammals.

PS Disclosure; Col 11; 45pp; English.
 XX
 CC The sequences given in AAR36937-78 are atrial natriuretic/vasodilator
 CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
 CC fluid volume and blood pressure in host organisms. These ANVP fragments
 CC may be produced by solid-phase techniques. See also AAR40387-749.
 CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
 CC correct PR field.)
 CC
 XX
 SQ Sequence 23 AA;
 XX
 Query Match 82.4%; Score 56; DB 2; Length 23;
 Best Local Similarity 58.8%; Pred. No. 0.00046;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 OY 1 CFGXXXDRIGXXSXGC 17
 ||| ||| |||
 DB 2 CFGARIDRIGAGSGLGC 18
 XX
 RESULT 26
 AAR36964
 ID AAR36964 standard; protein; 23 AA.
 XX
 AC AAR36964;
 XX
 DT 25-MAR-2003 (revised)
 DT 14-SEP-1993 (first entry)
 XX
 DE ANVP #28.
 XX
 KM Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 KM regulation; fluid volume; blood pressure.
 XX
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Disulfide-bond 2..18
 FT Misc-difference 15 /note= "D-form residue"
 XX
 PN US5212286-A.
 XX
 PD 18-MAY-1993.
 XX
 PF 05-JUN-1986; 86US-00870795.
 XX
 PR 19-APR-1984; 84US-00602117.
 PR 01-JUN-1984; 84US-00616488.
 PR 08-MAY-1985; 85US-00766030.
 XX
 PA (SCIO-) SCTOS NOVA INC.
 XX
 PI Lewicki JA, Scarborough RM;
 XX
 DR WPI, 1993-175525/21.
 XX
 PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
 XX in mammals.
 XX
 PS Disclosure; Col 10; 45pp; English.
 XX
 CC The sequences given in AAR36937-78 are atrial natriuretic/vasodilator
 CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
 CC fluid volume and blood pressure in host organisms. These ANVP fragments
 CC may be produced by solid-phase techniques. See also AAR40387-749.
 CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
 CC correct PR field.)
 CC
 XX
 SQ Sequence 23 AA;
 XX
 Query Match 82.4%; Score 56; DB 2; Length 23;
 Best Local Similarity 58.8%; Pred. No. 0.00046;

Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXSXXGC 17
 ||| ||| ||| |||
 DB 2 CFGGRIDRIGAGSALGC 18

RESULT 27

AA040427
 ID AA040427 standard; protein, 23 AA.

AA040427;
 AC

XX 25-MAR-2003 (revised)
 DT

DT 14-SEP-1993 (first entry)
 XX

DE [D-Ala132]rANVP(126-148)-NH₂.

XX Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.

XX Synthetic.

OS Key Location/Qualifiers

FH Disulfide-bond 4.20

FT Misc-difference 7 /note= "D-form residue"

FT Modified-site 23 /note= "Amidated C-terminal"

FT US5212286-A.

PN 18-MAY-1993.

XX 05-JUN-1986; 86US-00870795.

XX 19-APR-1984; 84US-00602117.

PR 01-JUN-1984; 84US-00616488.

PR 08-MAY-1985; 85US-00766030.

XX (SCIO-) SCIOS NOVA INC.

XX PI Lewicki JA, Scarborough RM;

XX WPI; 1993-175525/21.

XX New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator

XX in mammals.

XX Disclosure; Col 31; 45pp; English.

XX The sequences given in AA040387-748 are atrial natriuretic/ vasodilator

CC peptide (ANVP) CDNA's. These ANVP fragments may be used for regulation of

CC fluid volume and blood pressure in host organisms. These ANVP fragments

CC may be produced by solid-phase techniques. See also AA036937-78. (Updated

CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct

CC PR field.)

XX SQ Sequence 23 AA;

DB 1 CFGXXXXRIGXXSXXGC 17

DB 4 CFGARIDRIGAGSGLGC 20

RESULT 28

AA040622

ID AA040622 standard; protein; 23 AA.

AC AA040622;

XX 25-MAR-2003 (revised)

DT 14-SEP-1993 (first entry)

XX [Arg129] [D-Ala133]hANVP(130-151).

XX Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;

XX regulation; fluid volume; blood pressure.

XX Synthetic.

OS Key Location/Qualifiers

FH Disulfide-bond 2.18

FT Misc-difference 5 /note= "D form residue"

FT US5212286-A.

PN 18-MAY-1993.

XX 05-JUN-1986; 86US-00870795.

XX 19-APR-1984; 84US-00602117.

PR 01-JUN-1984; 84US-00616488.

PR 08-MAY-1985; 85US-00766030.

XX (SCIO-) SCIOS NOVA INC.

XX PI Lewicki JA, Scarborough RM;

XX WPI; 1993-175525/21.

XX New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator

XX in mammals.

XX Disclosure; Col 47; 45pp; English.

XX The sequences given in AA040387-748 are atrial natriuretic/ vasodilator

CC peptide (ANVP) CDNA's. These ANVP fragments may be used for regulation of

CC fluid volume and blood pressure in host organisms. These ANVP fragments

CC may be produced by solid-phase techniques. See also AA036937-78. (Updated

CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct

CC PR field.)

XX SQ Sequence 23 AA;

DB 1 CFGXXXXRIGXXSXXGC 17

DB 2 CFGARIDRIGAGSGLGC 18

RESULT 29

AA040625

ID AA040625 standard; protein; 23 AA.

AA040625;

XX 25-MAR-2003 (revised)

DT 14-SEP-1993 (first entry)

XX [Arg128] [D-Ala142]rANVP(129-150).

XX Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;

XX regulation; fluid volume; blood pressure.

XX Synthetic.

OS Key Location/Qualifiers

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FT Disulfide-bond 2. .18
FT Misc-difference 15
FT /note= "D form residue"
XX
XX US5212286-A.
XX
XX 18-MAY-1993.
XX
XX 05-JUN-1986; 86US-00870795.
XX
XX 19-APR-1984; 84US-00602117.
XX 01-JUN-1984; 84US-00616488.
XX 08-MAY-1985; 85US-00766030.
XX
XX (SCIO-) SCTOS NOVA INC.
XX
XX Lewicki JA, Scarborough RM;
XX
XX WPI; 1993-175525/21.
XX
XX New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
XX in mammals.
XX
XX Disclosure; Col 47; 45pp; English.
XX
XX
XX The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
XX peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
XX fluid volume and blood pressure in host organisms. These ANVP fragments
XX may be produced by solid-phase techniques. See also AAR36937-78. (Updated
XX on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct
XX PR field.)
XX
XX Sequence 23 AA:
SQ
Query Match 82.4%; Score 56; DB 2; Length 23;
Best Local Similarity 58.8%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 CFCGXXDRIGXXSXXGC 17
Db 2 CFCGRIDRIGQSAALGC 18
RESULT 30
AAR40628
ID AAR40628 standard; protein; 23 AA.
XX
XX AAR40628;
XX
XX 25-MAR-2003 (revised)
XX 14-SEP-1993 (first entry)
XX
XX [Arg129] [D-Ala143] hANVP(130-151).
XX
XX Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
XX regulation; fluid volume; blood pressure.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Disulfide-bond 2. .18
XX Misc-difference 15
XX /note= "D form residue"
XX
XX US5212286-A.
XX
XX 18-MAY-1993.
XX
XX 05-JUN-1986; 86US-00870795.
XX
XX 19-APR-1984; 84US-00602117.
XX 01-JUN-1984; 84US-00616488.
XX 08-MAY-1985; 85US-00766030.
XX

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XX
XX (SCIO-) SCTOS NOVA INC.
XX
XX Lewicki JA, Scarborough RM;
XX
XX WPI; 1993-175525/21.
XX
XX New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
XX in mammals.
XX
XX Disclosure; Col 48; 45pp; English.
XX
XX
XX The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
XX peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
XX fluid volume and blood pressure in host organisms. These ANVP fragments
XX may be produced by solid-phase techniques. See also AAR36937-78. (Updated
XX on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct
XX PR field.)
XX
XX Sequence 23 AA:
SQ
Query Match 82.4%; Score 56; DB 2; Length 23;
Best Local Similarity 58.8%; Pred. No. 0.00046;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 CFCGXXDRIGXXSXXGC 17
Db 2 CFCGRIDRIGQSAALGC 18
RESULT 31
AAR40619
ID AAR40619 standard; protein; 23 AA.
XX
XX AAR40619;
XX
XX 25-MAR-2003 (revised)
XX 14-SEP-1993 (first entry)
XX
XX [Arg129] [D-Ala132] rANVP(129-150).
XX
XX Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
XX regulation; fluid volume; blood pressure.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Disulfide-bond 2. .18
XX Misc-difference 5
XX /note= "D form residue"
XX
XX US5212286-A.
XX
XX 18-MAY-1993.
XX
XX 05-JUN-1986; 86US-00870795.
XX
XX 19-APR-1984; 84US-00602117.
XX 01-JUN-1984; 84US-00616488.
XX 08-MAY-1985; 85US-00766030.
XX
XX (SCIO-) SCTOS NOVA INC.
XX
XX Lewicki JA, Scarborough RM;
XX
XX WPI; 1993-175525/21.
XX
XX New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
XX in mammals.
XX
XX Disclosure; Col 47; 45pp; English.
XX
XX The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator

```

CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
 CC fluid volume and blood pressure in host organisms. These ANVP fragments
 CC may be produced by solid-phase techniques. See also AAR03304. (Updated
 CC on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct
 CC PR field.)

XX Sequence 23 AA;

Query Match 82.4%; Score 56; DB 2; Length 23;
 Best Local Similarity 58.8%; Pred. No. 0.00046;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXSXXGC 17
 DB 2 CFGARIDRIGAGSGMGC 18

RESULT 32

AAR03303
 ID AAR03303 standard; peptide; 24 AA.

XX AAR03303;
 AC AAR03303;
 XX 24-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 15-AUG-1990 (first entry)
 XX fANP-24 frog atrial natriuretic peptide.
 DE Atrial natriuretic peptide; fANP-24; diuretic; hypertensive.
 KW Rana catesbeiana.
 OS

XX Key Location/Qualifiers
 FH Disulfide-bond 4..20
 FT JP02025500-A.
 PN 26-JAN-1990.
 PD 14-JUL-1988; 88JP-00173740.
 PF 14-JUL-1988; 88JP-00173740.
 XX 14-JUL-1988; 88JP-00173740.
 PR (MATS/) MATSUO T.
 PA WPI; 1990-071805/10.
 DR
 XX New peptide with physiological activity - obtd. from heart of frog, has
 PT diuretic and antihypertensive properties.
 PS Claim 1; Fig 3; 8pp; Japanese.
 XX First three amino acids may be absent, see AAR03304. (Updated on 25-MAR-
 CC 2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS
 CC field)

XX Sequence 24 AA;

Query Match 82.4%; Score 56; DB 2; Length 24;
 Best Local Similarity 58.8%; Pred. No. 0.00048;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXSXXGC 17
 DB 4 CFGSRIDRIGAGSGMGC 20

RESULT 33

AAR04818
 ID AAR04818 standard; protein; 24 AA.

XX AAR04818;
 AC

XX 26-SEP-1990 (first entry)

DE Peptide with Agonist and antagonist activity to ANP.

KW ANP; agonist; antagonist; penicillamine.

OS Synthetic.

XX Key Location/Qualifiers
 FH Disulfide-bond 4..20
 FT Modified-site 4

FT /label= Cys D-Cys penicillamine or D-penicillamine
 FT /note= "AA 4 and 20 may not both be Cys."
 FT /label= Cys D-Cys penicillamine or D-penicillamine
 FT /note= "AA 4 and 20 may not both be Cys."

XX JP02096594-A.

PD 09-APR-1990.

XX 30-SEP-1988; 88JP-00246543.

XX 30-SEP-1988; 88JP-00246543.

XX (SUNR) SUNTORY LTD.

DR WPI; 1990-151858/20.

XX New peptide(s) with agonist and antagonist activity to ANP - contg. at
 PT least 15 amino-acid units and disulphide bridge.

XX Claim 4; Page 930; 24pp; Japanese.

XX Six N-terminal and five C-terminal acids may be shortened or absent

XX Sequence 24 AA;

Query Match 82.4%; Score 56; DB 2; Length 24;
 Best Local Similarity 58.8%; Pred. No. 0.00048;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXXRIGXXSXXGC 17
 DB 4 CFGSRIDRIGAGSGMGC 20

RESULT 34

AAR04813
 ID AAR04813 standard; protein; 24 AA.

XX AAR04813;

DT 26-SEP-1990 (first entry)

DE Peptide antagonistic to ANP.

KW Atrial natriuretic factor; antagonist.

OS Synthetic.

XX Key Location/Qualifiers
 FH Modified-site 4

FT /label= OTHER
 FT /note= "CH2NHCOMe, CH2CH2Q (where Q = 4-pyridyl) or 2-
 FT guinolylyl), CH2CONH2, CH2Ph, CH2COOH, SO3H,
 FT CH3, CH2CONHC8H17 ORCH2CH2NH2"
 FT 20

FT /label= OTHER
 FT /note= "CH2NHCOMe, CH2CH2Q (where Q = 4-pyridyl) or 2-
 FT guinolylyl), CH2CONH2, CH2Ph, CH2COOH, SO3H,
 FT CH3, CH2CONHC8H17 ORCH2CH2NH2"


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XX  JP02096595-A.
PN
XX
XX  09-APR-1990.
PD
XX  30-SEP-1988; 88JP-00246544.
PF
XX  30-SEP-1988; 88JP-00246544.
PR
XX  (SUNR ) SUNTORY LTD.
PA
XX  WPI; 1990-151659/20.
DR
XX  New peptide - has antagonistic activity against ANP.
PT
XX  Claim 4; Page 3; 14pp; Japanese.
PS
XX  See also AAR04811-14
CC
XX  Sequence 24 AA;
SQ

Query Match      82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy  1 CFCGXXDRIGXXSXXGC 17
    ||| ||| ||| |||
Db  4 CFCGRIDRIGAGSGMGC 20

RESULT 35
AAR0453
ID  AAR0453 standard; protein; 24 AA.
XX
AC  AAR0453;
XX
XX  25-MAR-2003 (revised)
DT
XX  14-SEP-1993 (first entry)
DE
XX  [D-A1a143]rANVP(127-150)-NH2.
XX
XX  Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
XX  regulation; fluid volume; blood pressure.
XX
XX  Synthetic.
OS
XX
XX  Key Location/Qualifiers
FH Disulfide-bond 4..20
FT Misc-difference 17
FT /note= "D-form residue"
FT Modified-site 24
FT /note= "Amidated C-terminal"
XX
XX  US5212286-A.
PN
XX  18-MAY-1993.
PD
XX  05-JUN-1986; 86US-00870795.
PF
XX  19-APR-1984; 84US-00602117.
PR 01-JUN-1984; 84US-00616488.
PR 08-MAY-1985; 85US-00766030.
XX
XX  (SCTIO-) SCTIOS NOVA INC.
PA
XX  Lewicki JA, Scarborough RM;
PI
XX  WPI; 1993-175525/21.
DR
XX
XX  New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
XX  in mammals.
PT
XX  Disclosure; Col 33; 45pp; English.
PS

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XX  The sequences given in AAR0387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX
XX  Sequence 24 AA;
SQ

Query Match      82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy  1 CFCGXXDRIGXXSXXGC 17
    ||| ||| ||| |||
Db  4 CFCGRMDRIGAGSALGC 20

RESULT 36
AAR0446
ID  AAR0446 standard; protein; 24 AA.
XX
AC  AAR0446;
XX
XX  25-MAR-2003 (revised)
DT
XX  14-SEP-1993 (first entry)
DE
XX  [D-A1a142]rANVP(126-149).
XX
XX  Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
XX  regulation; fluid volume; blood pressure.
XX
XX  Synthetic.
OS
XX
XX  Key Location/Qualifiers
FH Disulfide-bond 4..20
FT Misc-difference 17
FT /note= "D-form residue"
XX
XX  US5212286-A.
PN
XX  18-MAY-1993.
PD
XX  05-JUN-1986; 86US-00870795.
PF
XX  19-APR-1984; 84US-00602117.
PR 01-JUN-1984; 84US-00616488.
PR 08-MAY-1985; 85US-00766030.
XX
XX  (SCTIO-) SCTIOS NOVA INC.
PA
XX  Lewicki JA, Scarborough RM;
PI
XX  WPI; 1993-175525/21.
DR
XX
XX  New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
XX  in mammals.
PT
XX  Disclosure; Col 33; 45pp; English.
PS
XX
XX  The sequences given in AAR0387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX
XX  Sequence 24 AA;
SQ

Query Match      82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

QY 1 CFXGXXDRIGXXSXXGC 17
||| ||| ||| |||
DB 4 CFGGRDRIGAQSALGC 20

RESULT 37
ID AAR40432 standard; protein; 24 AA.
XX
AC AAR40432;
XX
XX
DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX
DE [D-Ala13]hANVP(127-150)-NH2.
XX
XX Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Disulfide-bond 4..20
FT Misc-difference 7
FT /note= "D-form residue"
FT Modified-site 24
FT /note= "Amidated C-terminal"

US5212286-A.
XX
PN 18-MAY-1993.
XX
PD 05-JUN-1986; 86US-00870795.
XX
PF 19-APR-1984; 84US-00602117.
XX PR 01-JUN-1984; 84US-00616488.
XX PR 08-MAY-1985; 85US-00766030.
XX
XX (SCTO-) SCTOS NOVA INC.
XX
XX PA
XX PI Lewicki JA, Scarborough RM;
XX WPI; 1993-175525/21.
XX
XX New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
PT in mammals.
PT
PS Disclosure; Col 32; 45pp; English.

XX The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX
XX
XX Sequence 24 AA;
SQ

Query Match 82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFXGXXDRIGXXSXXGC 17
||| ||| ||| |||
DB 4 CFGGRDRIGAQSALGC 20

RESULT 38
ID AAR40452 standard; protein; 24 AA.
XX
AC AAR40452;

XX
DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX
XX [D-Ala143]rANVP(127-150).
XX
XX Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Disulfide-bond 4..20
FT Misc-difference 17
FT /note= "D-form residue"

US5212286-A.
XX
PN 18-MAY-1993.
XX
PD 05-JUN-1986; 86US-00870795.
XX
PF 19-APR-1984; 84US-00602117.
XX PR 01-JUN-1984; 84US-00616488.
XX PR 08-MAY-1985; 85US-00766030.
XX
XX (SCTO-) SCTOS NOVA INC.
XX
XX PI Lewicki JA, Scarborough RM;
XX WPI; 1993-175525/21.
XX
XX New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
PT in mammals.
PT
PS Disclosure; Col 33; 45pp; English.

XX The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
CC fluid volume and blood pressure in host organisms. These ANVP fragments
CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX
XX
XX Sequence 24 AA;
SQ

Query Match 82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFXGXXDRIGXXSXXGC 17
||| ||| ||| |||
DB 4 CFGGRDRIGAQSALGC 20

RESULT 39
ID AAR40431 standard; protein; 24 AA.
XX
AC AAR40431;
XX
XX
DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX
DE [D-Ala133]hANVP(127-150).
XX
XX Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
KW regulation; fluid volume; blood pressure.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Disulfide-bond 4..20

FT Misc-difference 7 /note= "D-form residue"
 FT XX
 PN US5212286-A.
 XX
 PD 18-MAY-1993.
 XX
 PF 05-JUN-1986; 86US-00870795.
 XX
 PR 19-APR-1984; 84US-00602117.
 PR 01-JUN-1984; 84US-00616488.
 PR 08-MAY-1985; 85US-00766030.
 XX
 PA (SCIO-) SCIOS NOVA INC.
 XX
 PI Lewicki JA, Scarborough RM;
 XX
 DR WPI, 1993-175525/21.
 XX
 PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
 PT in mammals.
 XX
 PS Disclosure; Col 32; 45pp; English.
 XX
 CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
 CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
 CC fluid volume and blood pressure in host organisms. These ANVP fragments
 CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
 CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
 CC PR field.)
 CC XX
 SQ Sequence 24 AA;
 OY Query Match 82.4%; Score 56; DB 2; Length 24;
 Best Local Similarity 58.8%; Pred. No. 0.00048;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 DB 1 CPGXXXDRIGXXSXXGC 17
 4 CFGARMDRIGAOSGLGC 20
 RESULT 40
 AAR40425
 ID AAR40425 standard; protein; 24 AA.
 XX
 AC AAR40425;
 XX
 DT 25-MAR-2003 (revised)
 DT 14-SEP-1993 (first entry)
 XX
 DE [D-ALA132]rANVP(126-149).
 XX
 KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 4. .20
 FT Misc-difference 7 /note= "D-form residue"
 FT XX
 PN US5212286-A.
 XX
 PD 18-MAY-1993.
 XX
 PF 05-JUN-1986; 86US-00870795.
 XX
 PR 19-APR-1984; 84US-00602117.
 PR 01-JUN-1984; 84US-00616488.
 PR 08-MAY-1985; 85US-00766030.
 XX

PA (SCIO-) SCIOS NOVA INC.
 XX
 PI Lewicki JA, Scarborough RM;
 XX
 DR WPI, 1993-175525/21.
 XX
 PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
 PT in mammals.
 XX
 PS Disclosure; Col 31; 45pp; English.
 XX
 CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
 CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
 CC fluid volume and blood pressure in host organisms. These ANVP fragments
 CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
 CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
 CC PR field.)
 CC XX
 SQ Sequence 24 AA;
 OY Query Match 82.4%; Score 56; DB 2; Length 24;
 Best Local Similarity 58.8%; Pred. No. 0.00048;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 DB 1 CPGXXXDRIGXXSXXGC 17
 4 CFGARMDRIGAOSGLGC 20
 RESULT 41
 AAR40426
 ID AAR40426 standard; protein; 24 AA.
 XX
 AC AAR40426;
 XX
 DT 25-MAR-2003 (revised)
 DT 14-SEP-1993 (first entry)
 XX
 DE [D-ALA132]rANVP(126-149)-NH2.
 XX
 KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 4. .20
 FT Misc-difference 7 /note= "D-form residue"
 FT Modified-site 24 /note= "Amidated C-terminal"
 FT XX
 PN US5212286-A.
 XX
 PD 18-MAY-1993.
 XX
 PF 05-JUN-1986; 86US-00870795.
 XX
 PR 19-APR-1984; 84US-00602117.
 PR 01-JUN-1984; 84US-00616488.
 PR 08-MAY-1985; 85US-00766030.
 XX
 PA (SCIO-) SCIOS NOVA INC.
 XX
 PI Lewicki JA, Scarborough RM;
 XX
 DR WPI, 1993-175525/21.
 XX
 PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
 PT in mammals.
 XX
 PS Disclosure; Col 31; 45pp; English.
 XX

CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of fluid volume and blood pressure in host organisms. These ANVP fragments may be produced by solid-phase techniques. See also AAR36937-78. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 24 AA;

Query Match 82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17
Db 4 CFGARIDRIGASGLGC 20

RESULT 42

ID AAR40447 standard; protein; 24 AA.

AC AAR40447;

DT 25-MAR-2003 (revised)

DT 14-SEP-1993 (first entry)

DE [D-A1a142] rANVP (126-149) -NH2.

KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat; regulation; fluid volume; blood pressure.

OS Synthetic.

PH Key Location/Qualifiers

FT Disulfide-bond 4..20

FT Misc-difference 17

FT Modified-site 24 /note= "D-form residue"

FT /note= "Amidated C-terminal"

PN US5212286-A.

PD 18-MAY-1993.

PF 05-JUN-1986; 86US-00870795.

PR 19-APR-1984; 84US-00602117.

PR 01-JUN-1984; 84US-00616488.

PR 08-MAY-1985; 85US-00766030.

PA (SCIO-) SCTOS NOVA INC.

PI Lewicki JA, Scarborough RM;

DR WPI; 1993-175525/21.

PT New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator in mammals.

PS Disclosure; Col 33; 45pp; English.

XX The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of fluid volume and blood pressure in host organisms. These ANVP fragments may be produced by solid-phase techniques. See also AAR36937-78. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 24 AA;

Query Match 82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00048;

Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17
Db 4 CFGARIDRIGASGLGC 20

RESULT 43

ID AAW70091 standard; peptide; 24 AA.

AC AAW70091;

DT 28-OCT-1998 (first entry)

DE Atrial natriuretic peptide (ANP) sequence.

KW ANP; atrial natriuretic peptide; cardiac disease; cardiac hypertrophy; chronic heart failure; ischaemic cardiac disease; arrhythmia; cGMP; pulmonary blood circulation; haemodynamic property.

OS Unidentified.

PN WO9834636-A1.

PD 13-AUG-1998.

PF 05-FEB-1998; 98WO-JP000483.

PR 05-FEB-1997; 97JP-00022594.

PA (SUNR) SUNTORY LTD.

PI Inomata N, Yamaki A, Furuya M, Hidaka T;

DR WPI; 1998-446949/38.

PT Drug composition comprises natriuretic peptide(s) - for safe treatment of cardiac hypertrophy associated diseases and chronic heart failure.

PS Example; Page 23; 35pp; Japanese.

XX This represents an atrial natriuretic peptide (ANP) sequence. The CC invention provides a composition for treating cardiac diseases associated CC with cardiac hypertrophy. The composition comprises an active ingredient CC capable of binding to the peptide receptor of GC-A and promoting CC production of cGMP. The drug composition may be used clinically to treat CC cardiac diseases caused by cardiac hypertrophy, including chronic heart CC failure, ischaemic cardiac diseases and arrhythmia. The active substance CC can bind to the natriuretic peptide receptor of GC-A and promote CC production of cGMP, effectively preventing cardiac hypertrophy and CC leading to improvement of the pulmonary blood circulation. The substance CC does not affect haemodynamic properties, blood pressure, heart beat and CC urine volume

XX Sequence 24 AA;

Query Match 82.4%; Score 56; DB 2; Length 24;
Best Local Similarity 58.8%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CFGXXXDRIGXXSXGC 17
Db 4 CFGARIDRIGASGLGC 20

RESULT 44

ID AAB91295 standard; peptide; 24 AA.

AC AAB91295;

DT 22-JUN-2001 (first entry)

XX DE Atrial-natriuretic peptide (ANP) SEQ ID NO:471.
 XX XX
 XX DE Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KM blood component; modification; succinimidyl; maleimido group; amino;
 KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200069900-A2.
 PN
 PD 23-NOV-2000.
 PD
 PF 17-MAY-2000; 2000MO-US013576.
 PF
 PR 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 PR 15-OCT-1999; 99US-0159783P.
 XX
 XX (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 DR WPI; 2001-112059/12.
 XX
 XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX
 PS Disclosure; Page 353; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 24 AA;
 QY
 Query Match 82.4%; Score 56; DB 4; Length 24;
 Best Local Similarity 58.8%; Pred. No. 0.00048;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 DB 1 CFGXXXXRIGKXSXXGC 17
 4 CFGSRIDRIGAGSGWGC 20
 ID AAB91292 standard; peptide; 24 AA.
 ID AAB91292
 AC AAB91292;
 AC
 DT 22-JUN-2001 (first entry)
 DT
 XX Atrial-natriuretic peptide (ANP) SEQ ID NO:468.
 DE
 XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KM blood component; modification; succinimidyl; maleimido group; amino;
 KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX

XX OS Homo sapiens.
 OS Synthetic.
 PN WO200069900-A2.
 PN
 PD 23-NOV-2000.
 PD
 PF 17-MAY-2000; 2000MO-US013576.
 PF
 PR 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 PR 15-OCT-1999; 99US-0159783P.
 XX
 XX (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 DR WPI; 2001-112059/12.
 XX
 XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX
 PS Disclosure; Page 352; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 24 AA;
 QY
 Query Match 82.4%; Score 56; DB 4; Length 24;
 Best Local Similarity 58.8%; Pred. No. 0.00048;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 DB 1 CFGXXXXRIGKXSXXGC 17
 4 CFGSRIDRIGAGSGWGC 20
 ID AAE12435 standard; peptide; 24 AA.
 ID AAE12435
 AC AAE12435;
 AC
 DT 03-JAN-2002 (first entry)
 DT
 XX Frog atrial natriuretic peptide (ANP) #2.
 DE
 XX Prophylaxis; ischaemic heart disease; myocardial infarction; frog;
 KM ischaemia reperfusion injury; ischaemic heart disease; infarct region;
 KM vasotropic; atrial natriuretic peptide; ANP.
 XX
 OS Rana sp.
 OS
 XX Key Location/Qualifiers
 PH Disulfide-bond 4. .20
 XX

PN US2001027181-A1.
 PT 04-OCT-2001.
 XX
 PF 03-JAN-2001; 2001US-00752724.
 XX
 PR 31-MAR-2000; 2000JP-00098134.
 XX
 PA (KITA/) KITAKAZE M.
 XX
 PI Kitakaze M;
 XX
 DR WPI; 2001-638528/73.
 XX
 PT Composition for the treatment or prophylaxis of ischemic heart disease
 PT 1.e. myocardial infarction, comprises a substance which can increase
 PT intracellular cGMP production by acting on a natriuretic peptide
 PT receptor.
 XX
 PS Disclosure; Page 4; 9pp; English.
 XX
 CC The invention relates to a pharmaceutical composition for the treatment
 CC or prophylaxis of ischemic heart disease, comprises a substance as an
 CC active ingredient, which can increase intracellular cGMP production by
 CC acting on a natriuretic peptide receptor and which has an effect of
 CC reducing an infarct region. The composition is useful for suppressing
 CC ischaemia reperfusion injury in the treatment of ischemic heart disease,
 CC preferably myocardial infarction. The present sequence is frog atrial
 CC natriuretic peptide (ANP)
 XX
 SQ Sequence 24 AA:
 XX
 Query Match 82.4%; Score 56; DB 4; Length 24;
 Best Local Similarity 58.8%; Pred. No. 0.00048;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CFCGXXDRIGXXSXXGC 17
 Db 4 CFCGSRIDRIGAGSGWGC 20
 XX
 RESULT 47
 ADV86892
 ID ADV86892 standard; peptide; 24 AA.
 XX
 AC ADV86892;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE Bovine ANP peptide fragment.
 XX
 XX Immunosuppressive; Antirheumatic; Antiarthritic; Antidiabetic;
 KW Antiinflammatory; Anticancer; Gastrointestinal-Gen.; Neuroprotective;
 KW Antiproliferative; Dermatological; Muscular-Gen.; Thyromimetic;
 KW guanosine monophosphate; GMP; Guanylyl cyclase A-modulator;
 KW atrial natriuretic peptide; ANP; immune disorder;
 KW cerebral natriuretic peptide.
 XX
 OS Bos sp.
 OS
 PN WO2004110489-A1.
 XX
 PD 23-DEC-2004.
 XX
 PF 11-JUN-2004; 2004WO-JP008205.
 XX
 PR 13-JUN-2003; 2003JP-00169370.
 XX
 PA (SUNR) DAICHI SUNTORY PHARMA CO LTD.
 XX
 PI Horl T;
 XX
 DR WPI; 2005-066084/07.

XX
 PT Composition comprising natriuretic-peptide acting on guanylyl cyclase A
 PT and enhancing cyclic guanosine monophosphate production, useful for
 PT prevention/treatment of Th1-type immunological disease e.g., autoimmune
 PT disease.
 XX
 PS Disclosure; SEQ ID NO 5; 32pp; Japanese.
 XX
 CC This sequence represents a fragment of an atrial natriuretic-peptide.
 CC This peptide may be used in a pharmaceutical composition for prevention
 CC or treatment of Th1-type immunological disease. The composition comprises
 CC a substance capable of acting on guanylyl cyclase A, which is a
 CC natriuretic-peptide receptor and enhancing cyclic guanosine monophosphate
 CC production, as an active ingredient. The claimed substance may be used
 CC for controlling Th1/Th2 balance in the immune system to induce Th2
 CC deflection property. In the claimed composition, the guanylyl cyclase A
 CC is natriuretic-peptide receptor. The substance is a natriuretic-peptide
 CC which is an atrial or cerebral natriuretic-peptide. The atrial
 CC natriuretic-peptide is preferably of human origin. The enhancement of
 CC cyclic guanosine monophosphate (cGMP) production by atrial natriuretic-
 CC peptide (ANP) was determined in vitro. RNA was synthesized from the
 CC monocyte obtained from the peripheral blood of a healthy subject. The
 CC dendritic cells were allowed to react with ANP and with cerebral
 CC natriuretic peptide (CNP) (control). The ANP raised cGMP in dendritic
 CC cell at a higher concentration of 10-12 M than in monocytes. CNP did not
 CC influence intracellular cGMP concentration in monocytes or dendritic
 CC cells. The composition is useful for preventing or treating Th1-type
 CC immunological disease chosen from graft-versus-host disease, autoimmune
 CC disease, disease resulting from bone marrow transplant and immunological
 CC disease resulting from transplant rejection. The autoimmune disease are
 CC autoimmune hepatitis, rheumatoid arthritis, insulin-dependent diabetes
 CC mellitus, ulcerative colitis, Crohns' disease, multiple sclerosis,
 CC autoimmune myocarditis, psoriasis, scleroderma, myasthenia gravis,
 CC multiple myeloma, dermatomyositis, Hashimoto's disease, autoimmune
 CC hypothyroidism (erythroblastosis, hypoplastic anemia, etc.), Sjogrens 's
 CC syndrome, angitis syndrome and systemic lupus erythematosus, preferably
 CC Crohns' disease or multiple sclerosis. The claimed substance is useful
 CC for treating Th1-type immunological disease, for manufacturing a
 CC pharmaceutical composition for preventing or treating Th1-type
 CC immunological disease, and for controlling Th1/Th2 balance in the immune
 CC system. The claimed composition enables control of Th1/Th2 balance in an
 CC immune system by using the substance which acts on guanylyl cyclase A.
 CC Note: This sequence is not given in the specification.
 XX
 SQ Sequence 24 AA:
 XX
 Query Match 82.4%; Score 56; DB 9; Length 24;
 Best Local Similarity 58.8%; Pred. No. 0.00048;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CFCGXXDRIGXXSXXGC 17
 Db 4 CFCGSRIDRIGAGSGWGC 20
 XX
 RESULT 48
 AAR40424
 ID AAR40424 standard; protein; 25 AA.
 XX
 AC AAR40424;
 XX
 DT 25-MAR-2003 (revised)
 DT 14-SEP-1993 (first entry)
 XX
 DE [D-A1a132] rANVP (126-150)-NH2.
 XX
 KW Human, pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 KW regulation; fluid volume; blood pressure.
 XX
 OS Synthetic.
 OS
 PI Key Location/Qualifiers
 PH Disulfide-bond 4..20
 FT

FT Misc-difference 7 /note= "D-form residue"
 FT Modified-site 25 /note= "Amidated C-terminal"
 FT
 XX US5212286-A.
 PN 18-MAY-1993.
 XX
 PD 05-JUN-1986; 86US-00870795.
 XX
 PF 19-APR-1984; 84US-00602117.
 PR 01-JUN-1984; 84US-00616488.
 PR 08-MAY-1985; 85US-00766030.
 XX
 PA (SCTO-) SCTOS NOVA INC.
 XX
 PI Lewicki JA, Scarborough RM;
 XX WPI, 1993-175525/21.
 DR
 XX New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
 PT in mammals.
 FT
 XX
 PS Disclosure; Col 31; 45pp; English.
 XX
 CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
 CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
 CC fluid volume and blood pressure in host organisms. These ANVP fragments
 CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
 CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
 CC PR field.)
 CC
 XX
 SQ Sequence 25 AA;

Query Match 82.4%; Score 56; DB 2; Length 25;
 Best Local Similarity 58.8%; Pred. No. 0.0005;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFCGXXDRIGXXSXGC 17
 ||| ||| ||| |||
 DB 4 CFCARIDRIGAGSGIGC 20

RESULT 49

AAR40587
 ID AAR40587 standard; protein; 25 AA.
 XX

AC AAR40587;
 XX

DT 25-MAR-2003 (revised)
 DT 14-SEP-1993 (first entry)
 XX

DE [A1A132] rANVP (126-150).
 XX

KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 regulation; fluid volume; blood pressure.
 KM
 XX

OS Synthetic.
 OS

FT Key Location/Qualifiers
 FT Disulfide-bond 4..20
 XX

PN US5212286-A.
 XX

PD 18-MAY-1993.
 XX

PF 05-JUN-1986; 86US-00870795.
 XX

PR 19-APR-1984; 84US-00602117.
 PR 01-JUN-1984; 84US-00616488.
 PR 08-MAY-1985; 85US-00766030.
 XX

PA (SCTO-) SCTOS NOVA INC.
 XX
 PI Lewicki JA, Scarborough RM;
 XX WPI, 1993-175525/21.
 XX
 DR New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
 PT in mammals.
 FT
 XX
 PS Disclosure; Col 44; 45pp; English.
 XX
 CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
 CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
 CC fluid volume and blood pressure in host organisms. These ANVP fragments
 CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
 CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
 CC PR field.)
 CC
 XX
 SQ Sequence 25 AA;

Query Match 82.4%; Score 56; DB 2; Length 25;
 Best Local Similarity 58.8%; Pred. No. 0.0005;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CFCGXXDRIGXXSXGC 17
 ||| ||| ||| |||
 DB 4 CFCARIDRIGAGSGIGC 20

RESULT 50

AAR40451
 ID AAR40451 standard; protein; 25 AA.
 XX

AC AAR40451;
 XX

DT 25-MAR-2003 (revised)
 DT 14-SEP-1993 (first entry)
 XX

DE [D-A1A143] rANVP (127-151)-NH2.
 XX

KW Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
 regulation; fluid volume; blood pressure.
 KM
 XX

OS Synthetic.
 OS

FT Key Location/Qualifiers
 FT Disulfide-bond 4..20
 FT Misc-difference 17
 FT Modified-site 25 /note= "D-form residue"
 FT /note= "Amidated C-terminal"
 XX

PN US5212286-A.
 XX

PD 18-MAY-1993.
 XX

PF 05-JUN-1986; 86US-00870795.
 XX

PR 19-APR-1984; 84US-00602117.
 PR 01-JUN-1984; 84US-00616488.
 PR 08-MAY-1985; 85US-00766030.
 XX

PA (SCTO-) SCTOS NOVA INC.
 XX

PI Lewicki JA, Scarborough RM;
 XX WPI, 1993-175525/21.
 DR

PF New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator
 FT in mammals.
 FT
 XX

PS Disclosure; Col 33; 45pp; English.
 XX

CC The sequences given in AAR40387-748 are atrial natriuretic/ vasodilator
 CC peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of
 CC fluid volume and blood pressure in host organisms. These ANVP fragments
 CC may be produced by solid-phase techniques. See also AAR36937-78. (Updated
 CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
 CC PR field.)
 CC
 CC
 CC

XX
 SQ Sequence 25 AA:

Query Match 82.4%; Score 56; DB 2; Length 25;
 Best Local Similarity 58.8%; Pred. No. 0.0005;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CPGXXXDRIGXXXGC 17
 ||| ||| |
 Db 4 CPGGRMDRIGAQSGALGC 20

Search completed: January 26, 2006, 14:43:41
 Job time : 84 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 26, 2006, 14:39:17 : Search time 17 Seconds

(without alignments)
96.217 Million cell updates/sec

Title: US-10-664-605-5

Perfect score: 68

Sequence: 1 CFGXXXXRIGXXXXGC 17

Scoring table: BLOSUM62

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database : PIR 80:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Listing first 1000 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	82.4	30	2	S01657
2	56	82.4	128	2	S14872
3	56	82.4	145	1	JQ0947
4	55	80.9	22	2	JT0581
5	55	80.9	22	2	A35418
6	55	80.9	22	2	A36399
7	55	80.9	27	2	JC1081
8	55	80.9	27	2	A33431
9	55	80.9	36	2	S15821
10	55	80.9	38	2	S71381
11	55	80.9	103	2	A41403
12	55	80.9	105	2	B35736
13	55	80.9	115	1	S15822
14	55	80.9	118	2	B54119
15	55	80.9	121	1	A30162
16	55	80.9	121	2	A49144
17	55	80.9	121	2	I49548
18	55	80.9	126	1	A35155
19	55	80.9	126	1	AMHUC
20	55	80.9	126	1	A55688
21	55	80.9	126	2	S12988
22	55	80.9	129	1	A54119
23	55	80.9	131	2	A31676
24	55	80.9	131	2	A33873
25	55	80.9	135	1	A61244
26	55	80.9	140	1	S14320
27	55	80.9	140	1	AMDG
28	55	80.9	150	1	S13107
29	55	80.9	151	1	AMHU

30	55	80.9	152	1	AMBO	atrial natriuretic
31	55	80.9	152	1	AMMS	atrial natriuretic
32	55	80.9	152	1	AMRT	atrial natriuretic
33	55	80.9	153	1	AMRB	atrial natriuretic
34	55	80.9	153	2	S14873	atrial natriuretic
35	55	80.9	161	4	I55480	hypothetical natri
36	50	73.5	134	1	AMHUB	natriuretic peptid
37	48	70.6	38	2	A42974	natriuretic peptid
38	37	54.4	167	2	T18196	pol protein - s1lk
39	36	52.9	541	2	T34850	probable acid-CoA
40	35	51.5	113	2	S66859	hypothetical prote
41	35	51.5	2110	2	B44110	mycocerosate synth
42	35	51.5	2111	2	A70668	mycocerosate synth
43	35	51.5	2116	2	C86926	probable mycoceros
44	35	51.5	2118	2	S72705	mycocerosate synth
45	34	50.0	327	2	A11422	hypothetical prote
46	34	50.0	504	2	H97462	hypothetical prote
47	34	50.0	648	2	S50856	whn protein - rat
48	34	50.0	2108	2	H70819	probable polyketid
49	33	48.5	137	2	A97088	uncharacterized pr
50	33	48.5	419	2	T10652	hypothetical prote
51	33	48.5	472	1	WMADP6	early E1B 52K prot
52	33	48.5	475	1	WMADP6	early E1B 52K prot
53	32	47.1	66	2	T43057	spermiogenesis pro
54	32	47.1	315	2	T33059	hypothetical prote
55	32	47.1	347	2	T02669	hypothetical prote
56	32	47.1	411	2	A87390	transporter, proba
57	32	47.1	433	2	AG0831	alpha-ketoglutarat
58	32	47.1	437	2	H83175	probable MFS trans
59	32	47.1	446	2	A42661	citrate carrier pr
60	32	47.1	446	2	AD0509	citrate-sodium sym
61	32	47.1	446	2	B42661	citrate carrier pr
62	32	47.1	462	2	D83117	probable MFS trans
63	32	47.1	488	2	H90423	sugar transport pr
64	32	47.1	509	2	JH0501	zinc finger protei
65	32	47.1	519	2	T45764	hypothetical prote
66	32	47.1	566	2	S14777	hypothetical prote
67	32	47.1	1871	2	A87204	polyketide synthas
68	31	45.6	260	2	A83457	conserved hypotet
69	31	45.6	286	2	AG3276	protein erik/stik
70	31	45.6	286	2	T36988	probable secreted
71	31	45.6	369	2	C97484	outer membrane pro
72	31	45.6	369	2	AC2702	hypothetical prote
73	31	45.6	387	2	F84392	transporter homolo
74	31	45.6	400	2	C69757	hypothetical prote
75	31	45.6	407	2	C64167	aspartate transam
76	31	45.6	412	1	XNCHDC	dicarboxylic acid
77	31	45.6	432	2	A83616	probable transmemb
78	31	45.6	450	2	F95360	probable metabolit
79	31	45.6	454	2	AC0444	hypothetical major
80	31	45.6	454	2	AD0556	probable transport
81	31	45.6	456	1	C64772	probable transport
82	31	45.6	456	2	B85539	probable transport
83	31	45.6	456	2	A90689	probable transport
84	31	45.6	456	2	A10384	probable transport
85	31	45.6	462	2	A97782	phosphomannomutase
86	31	45.6	469	2	F64163	3-isopropylmalate
87	31	45.6	482	2	T30983	hypothetical prote
88	31	45.6	495	2	AF1827	alpha, alpha-crenal
89	31	45.6	532	2	A96792	probable phosphate
90	31	45.6	872	2	AC2134	ferriheme-iron r
91	31	45.6	1582	2	E70876	probable polyketid
92	31	45.6	1890	2	T04556	hypothetical prote
93	31	45.6	2220	2	A45290	calcium channel pr
94	30	44.1	137	2	B83475	hypothetical prote
95	30	44.1	172	2	E72472	hypothetical prote
96	30	44.1	211	2	G70981	hypothetical prote
97	30	44.1	252	1	MEIVIF	matrix protein M1
98	30	44.1	258	2	H96013	conserved hypotet
99	30	44.1	264	2	T37551	hypothetical prote
100	30	44.1	270	2	D71301	hypothetical prote
101	30	44.1	307	2	AF2402	hypothetical prote
102	30	44.1	320	2	A53119	cell adhesion glyco

103	30	44.1	353	2	S37873	hypothetical prote
104	30	44.1	354	2	S60242	cinamyl alcohol d
105	30	44.1	366	2	B86341	hypothetical prote
106	30	44.1	397	2	S27600	N-acetylglutamate
107	30	44.1	398	1	D64464	hypothetical prote
108	30	44.1	406	2	C84940	3-oxoacyl-l-acyl-ca
109	30	44.1	409	2	A84602	hypothetical prote
110	30	44.1	414	2	H95999	probable N-carbamyl
111	30	44.1	427	2	G85719	probable transport
112	30	44.1	427	2	B64909	probable membrane
113	30	44.1	427	2	H90897	probable membrane
114	30	44.1	429	2	T08562	hypothetical prote
115	30	44.1	459	2	AE0679	probable membrane
116	30	44.1	469	2	B81395	probable MFS trans
117	30	44.1	471	2	H90502	phosphate transport
118	30	44.1	495	2	A95984	probable xanthine
119	30	44.1	514	2	B96585	hypothetical prote
120	30	44.1	521	2	S67491	phosphate transpor
121	30	44.1	566	2	A72329	general secretion
122	30	44.1	645	2	AE2655	conserved hypothet
123	30	44.1	672	2	A97437	hypothetical 71.3K
124	30	44.1	683	2	C71322	probable translati
125	30	44.1	830	2	B83031	conserved hypothet
126	30	44.1	861	2	B49847	nitrate reductase
127	30	44.1	863	2	D88216	protein B0495.7 [i
128	30	44.1	863	1	I38908	UV-damaged DNA-bin
129	30	44.1	1140	1	S38777	UV-damaged DNA-bin
130	30	44.1	1140	1	JC7152	UV-damaged DNA-bin
131	30	44.1	1331	1	XORTDH	xanthine dehydroge
132	30	44.1	1335	1	XOMSDH	xanthine dehydroge
133	30	44.1	2514	2	T37320	ataxia telangiectra
134	30	44.1	2619	2	T24588	hypothetical prote
135	29	42.6	121	2	A49590	Ig heavy chain V r
136	29	42.6	137	2	G97352	unc characterized co
137	29	42.6	145	2	A81992	hypothetical prote
138	29	42.6	165	2	B81222	hypothetical prote
139	29	42.6	265	2	D83577	conserved hypothet
140	29	42.6	344	2	C82511	hypothetical prote
141	29	42.6	349	2	H75468	conserved hypothet
142	29	42.6	357	2	T29856	probable aspartate
143	29	42.6	362	2	A70547	probable mena - My
144	29	42.6	368	2	B87191	o-succinylbenzoic
145	29	42.6	371	2	B90267	transport protein,
146	29	42.6	378	2	T25985	hypothetical prote
147	29	42.6	399	2	D83535	aromatic amino aci
148	29	42.6	399	2	T23470	hypothetical prote
149	29	42.6	414	1	D82487	multidrug resistan
150	29	42.6	419	1	DEECNB	glycerol-3-phospha
151	29	42.6	419	2	A85864	hypothetical prote
152	29	42.6	419	2	G91019	hypothetical prote
153	29	42.6	422	2	C70518	probable nant proc
154	29	42.6	431	2	D83160	nitrite extrusion
155	29	42.6	434	2	G97610	hypothetical metab
156	29	42.6	434	2	AC2833	hypothetical prote
157	29	42.6	438	2	G64962	shikimate transport
158	29	42.6	438	2	B90976	shikimate transport
159	29	42.6	438	2	H85822	probable transport
160	29	42.6	440	2	AD0986	hypothetical metab
161	29	42.6	440	2	S47743	probable sugar tra
162	29	42.6	440	2	D86025	probable transport
163	29	42.6	440	2	C91179	probable transport
164	29	42.6	455	2	AD1329	UDP-N-acetylmuram
165	29	42.6	455	2	AD1700	UDP-N-acetylmuram
166	29	42.6	481	2	G82125	Na+/H+ antiporter
167	29	42.6	498	2	T20646	antitranilate synth
168	29	42.6	504	2	AG1847	antitranilate synth
169	29	42.6	508	2	G71654	phosphomannomutase
170	29	42.6	536	2	T19488	hypothetical prote
171	29	42.6	538	2	D69165	hypothetical prote
172	29	42.6	627	2	B48442	membrane transport
173	29	42.6	645	2	F70825	probable PPE prote
174	29	42.6	654	2	T34613	NADH2 dehydrogenas
175	29	42.6	671	2	S61693	probable membrane
176	176	42.6	737	2	T46101	ABC transporter-11
177	177	42.6	819	2	C64615	hypothetical prote
178	178	42.6	867	2	T02579	hypothetical prote
179	29	42.6	1517	1	F65112	glutamate synthase
180	29	42.6	1517	2	F85985	glutamate synthase
181	29	42.6	1517	2	C91140	glutamate synthase
182	29	42.6	1588	2	T38660	probable transcrip
183	29	42.6	1701	2	T43213	ENBP1 protein - ba
184	29	42.6	2126	2	E70522	probable polyketid
185	28.5	41.2	426	2	C84202	hypothetical prote
186	28	41.2	75	2	AC3445	H+-transporting tw
187	28	41.2	83	2	T35495	hypothetical prote
188	28	41.2	83	2	A45466	glycine/tyrosine-r
189	28	41.2	144	2	T44915	superoxide dismuta
190	28	41.2	152	2	B97865	proline/betaine tr
191	28	41.2	180	2	B95966	hypothetical prote
192	28	41.2	189	2	S04670	hypothetical prote
193	28	41.2	197	2	AE2808	succinoglycan bios
194	28	41.2	224	2	D70665	probable urease ac
195	28	41.2	224	2	C97587	succinoglycan bios
196	28	41.2	231	2	H66463	F12612.17 protein
197	28	41.2	235	2	D87629	transcription regu
198	28	41.2	235	2	H97197	unc characterized pr
199	28	41.2	241	2	T31573	hypothetical prote
200	28	41.2	258	2	C64108	hypothetical prote
201	28	41.2	286	2	AC6905	2-oxoglutarate syn
202	28	41.2	291	2	AC1302	hypothetical prote
203	28	41.2	291	2	AC1674	hypothetical prote
204	28	41.2	291	2	H84811	hypothetical prote
205	28	41.2	298	2	F81303	branched-chain am
206	28	41.2	333	2	B42476	hypothetical prote
207	28	41.2	333	2	AC0766	probable glycosyl
208	28	41.2	349	2	H35470	Wnt-7b protein m
209	28	41.2	357	2	H87378	phenylalaninyl-CNA
210	28	41.2	397	2	AC2110	hypothetical prote
211	28	41.2	402	2	B69783	bicyclic mycin resis
212	28	41.2	402	2	B75639	probable multidrug
213	28	41.2	412	2	S13035	aspartate transam
214	28	41.2	413	2	S28028	aspartate transam
215	28	41.2	413	2	JT0439	aspartate transam
216	28	41.2	413	2	S29027	aspartate transam
217	28	41.2	419	2	S01076	aspartate transam
218	28	41.2	419	2	D71112	hypothetical prote
219	28	41.2	415	2	D71647	proline/betaine tr
220	28	41.2	418	2	T39279	probable homocitra
221	28	41.2	419	2	A81258	alpha-ketoglutarat
222	28	41.2	419	2	JO1201	CmlA protein - Pae
223	28	41.2	425	2	A47033	chloramphenicol re
224	28	41.2	425	2	F70608	hypothetical prote
225	28	41.2	428	2	S58735	homocitrate synth
226	28	41.2	431	2	B96006	probable metabolit
227	28	41.2	431	2	D81282	probable efflux pr
228	28	41.2	433	2	H90495	metabolite transpo
229	28	41.2	433	2	B98095	type III secretion
230	28	41.2	439	2	F85940	type III secretion
231	28	41.2	440	1	S67674	homocitrate synth
232	28	41.2	440	2	E95352	probable MbA prot
233	28	41.2	457	2	AF3321	alpha-ketoglutarat
234	28	41.2	466	2	G89825	hypothetical prote
235	28	41.2	472	2	T34748	transmembrane tran
236	28	41.2	472	2	F82639	resistance protein
237	28	41.2	475	2	T45766	hypothetical prote
238	28	41.2	478	2	T33985	hypothetical prote
239	28	41.2	482	2	S63659	NADH2 dehydrogenas
240	28	41.2	488	2	F95050	NADH2 dehydrogenas
241	28	41.2	488	2	B97921	glutamy1-CrNA (Gln)
242	28	41.2	491	2	AB1722	glutamy1-CrNA (Gln)
243	28	41.2	491	2	F71568	lysyl-CrNA synthet
244	28	41.2	495	2	F89818	probable glu-CrNA
245	28	41.2	506	2	H71253	probable secreted
246	28	41.2	524	2	A29600	alkaline phosphata
247	28	41.2	524	2	S66467	alkaline phosphata
248	28	41.2	524	2		

249	28	41.2	528	2	T30132	hypothetical prote	322	27	39.7	303	2	B96909	probable permease
250	28	41.2	556	2	G88941	protein R13D1.8 [323	27	39.7	304	2	S67148	hypothetical prote
251	28	41.2	609	2	T45497	transpositional prot	324	27	39.7	307	2	A71807	hypothetical prote
252	28	41.2	624	1	RDYCS7	sulfite reductase	325	27	39.7	307	2	UC5036	hypothetical prote
253	28	41.2	624	2	T49366	myocyte-specific e	326	27	39.7	311	2	E71206	hypothetical prote
254	28	41.2	650	2	A11974	ferredoxin-sulfite	327	27	39.7	307	2	T32860	hypothetical prote
255	28	41.2	664	2	D82056	ABC transporter, A	328	27	39.7	326	2	T51060	hypothetical prote
256	28	41.2	687	2	JO1044	arylhporin precurs	329	27	39.7	326	2	A33755	myb-induced myeloi
257	28	41.2	691	2	P91251	probable tape meas	330	27	39.7	333	2	G81132	hypothetical prote
258	28	41.2	717	2	T34514	hypothetical prote	331	27	39.7	333	2	H81888	hypothetical prote
259	28	41.2	747	2	F69332	heterodisulfide re	332	27	39.7	337	2	S60577	porphobilinogen sy
260	28	41.2	757	2	F83516	hypothetical prote	333	27	39.7	338	2	E82432	hypothetical prote
261	28	41.2	783	2	E96652	protein F23M19.11	334	27	39.7	339	2	B86577	hypothetical prote
262	28	41.2	787	2	S35701	translation elonga	335	27	39.7	339	2	C72048	tptr repeats-ct683
263	28	41.2	818	2	S62790	misamatch DNA recog	336	27	39.7	341	2	T31826	hypothetical prote
264	28	41.2	831	2	T15108	hypothetical prote	337	27	39.7	347	2	G75283	asparaginase (EC 3
265	28	41.2	870	2	B40121	Grpase-activating	338	27	39.7	350	2	A82798	hypothetical prote
266	28	41.2	880	2	S51473	probable membrane	339	27	39.7	352	2	AB2248	N-acetyl-L-glutamate
267	28	41.2	928	2	S40745	hypothetical prote	340	27	39.7	356	2	H90289	permease, sugar tr
268	28	41.2	975	2	C81728	metalloproteinase,	341	27	39.7	363	2	T19527	hypothetical prote
269	28	41.2	996	1	S43208	NAD ADP-ribosyltra	342	27	39.7	374	2	F90361	transport membrane
270	28	41.2	1010	2	G88554	protein F54C8.3 [l	343	27	39.7	375	1	A48257	alcohol dehydrogen
271	28	41.2	1038	2	UT0663	ras Grpase-activa	344	27	39.7	375	1	I60970	alcohol dehydrogen
272	28	41.2	1044	2	S01966	Grpase-activating	345	27	39.7	375	1	I60973	alcohol dehydrogen
273	28	41.2	1047	2	A40121	Grpase-activating	346	27	39.7	376	2	S40470	mitogen-activated
274	28	41.2	1126	1	MMFM12	125k protein - alf	347	27	39.7	387	2	B90862	probable membrane
275	28	41.2	1148	2	T09073	splicing factor Sif	348	27	39.7	397	2	F70001	multidrug resistan
276	28	41.2	1333	2	T04251	P-glycoprotein 2 -	349	27	39.7	400	2	C82503	hypothetical prote
277	28	41.2	1486	2	A10906	glutamate synthase	350	27	39.7	412	2	I39551	phosphoglycerate k
278	28	41.2	1489	2	A82524	glutamate synthase	351	27	39.7	413	2	I39551	phosphoglycerate k
279	28	41.2	1496	2	B81416	glutamate synthase	352	27	39.7	423	2	S74046	probable sugar tra
280	28	41.2	1538	2	AF0432	glutamate synthase	353	27	39.7	425	2	S65504	hypothetical 46.6K
281	28	41.2	2480	2	D84904	hypothetical prote	354	27	39.7	426	2	C90425	metabolite transpo
282	28	41.2	3164	1	WMBE66	UL3 protein - hum	355	27	39.7	426	2	AB3582	metabolite transpo
283	27.5	40.4	367	2	T39574	probable uracil Ki	356	27	39.7	427	2	B90371	transpo
284	27.5	40.4	434	2	T01013	hypothetical prote	357	27	39.7	427	2	G69067	N-ethylmaleimide ch
285	27.5	40.4	2437	2	S42612	transmembrane prot	358	27	39.7	431	2	A70588	probable mbtg prot
286	27	39.7	35	2	F83051	hypothetical prote	359	27	39.7	438	2	A64147	hypothetical prote
287	27	39.7	80	2	E83102	conserved hypothet	360	27	39.7	439	2	D86297	hypothetical prote
288	27	39.7	103	2	AG0237	probable cytochrom	361	27	39.7	443	2	H85485	probable transport
289	27	39.7	104	2	T47010	hypothetical prote	362	27	39.7	443	2	H90634	probable transport
290	27	39.7	128	2	I51603	gene Xcat-2 protei	363	27	39.7	443	2	E64725	yaau protein - Bac
291	27	39.7	133	2	S10038	hypothetical prote	364	27	39.7	446	2	B90463	proline/betaine tr
292	27	39.7	147	2	AH1021	conserved hypothet	365	27	39.7	448	1	A22830	benzene 1,2-dioxyg
293	27	39.7	152	2	H97405	hypothetical prote	366	27	39.7	448	2	H70947	hypothetical prote
294	27	39.7	163	2	S40924	hypothetical prote	367	27	39.7	454	2	F75580	probable sugar tra
295	27	39.7	178	2	D69467	probable orotate p	368	27	39.7	460	2	T35916	conserved hypothet
296	27	39.7	180	2	S18119	male protein homol	369	27	39.7	466	2	T07404	probable glucosylt
297	27	39.7	187	2	E72390	orotate phosphorib	370	27	39.7	470	2	S78440	phosphoglucumutase
298	27	39.7	192	2	B82232	thymidine kinase (371	27	39.7	473	2	H86240	hypothetical prote
299	27	39.7	196	2	D70470	conserved hypothet	372	27	39.7	475	2	A86811	beta-glucosidase (
300	27	39.7	196	2	AD0265	thymidine kinase (373	27	39.7	477	2	S50738	Orl1 protein - yea
301	27	39.7	206	2	G82893	urease complex com	374	27	39.7	478	2	A72721	probable Glycerol
302	27	39.7	223	2	B96506	hypothetical prote	375	27	39.7	484	2	E82248	hypothetical prote
303	27	39.7	226	2	C82124	oxidoreductase, sh	376	27	39.7	484	2	B64481	hypothetical prote
304	27	39.7	230	2	AD0894	conserved hypothet	377	27	39.7	485	2	F97228	glu-tRNAgin amidot
305	27	39.7	239	2	H72667	hypothetical prote	378	27	39.7	486	2	S30959	gene 14 protein -
306	27	39.7	239	2	H85756	partial probable m	379	27	39.7	496	2	T19776	hypothetical prote
307	27	39.7	259	2	C36819	C11 protein - rabb	380	27	39.7	498	2	B86436	protein F17F8.1 (i
308	27	39.7	262	2	T47607	hypothetical prote	381	27	39.7	500	2	T49388	related to ascus d
309	27	39.7	263	2	T50596	probable oxidoreu	382	27	39.7	501	2	G83848	cobyrlic acid synth
310	27	39.7	272	2	T08762	hypothetical prote	383	27	39.7	501	2	UC7877	toxlin-60A - Okinaw
311	27	39.7	272	2	T14755	hypothetical prote	384	27	39.7	502	2	T00483	hypothetical prote
312	27	39.7	272	2	D87436	2-Keto-4-pentenat	385	27	39.7	504	2	A83901	hypothetical prote
313	27	39.7	273	2	A84356	ATP-binding protei	386	27	39.7	505	2	AB3134	chlorohydroxylase (i
314	27	39.7	282	2	H81358	probable signal pe	387	27	39.7	505	2	B98154	hypothetical prote
315	27	39.7	283	2	T46514	pathway-specific t	388	27	39.7	509	2	D84339	L-aspartate oxidas
316	27	39.7	283	2	D66143	hypothetical prote	389	27	39.7	510	2	T07119	cytochrome P450 CP
317	27	39.7	284	2	B64694	conserved hypothet	390	27	39.7	516	2	E86062	probable 2-compone
318	27	39.7	284	2	T34275	hypothetical prote	391	27	39.7	516	2	D91216	hypothetical 56.2K
319	27	39.7	292	2	G71701	succinate-CoA liga	392	27	39.7	517	2	AC2237	uroporphyrinogen I
320	27	39.7	293	2	A12775	conserved hypothet	393	27	39.7	517	2	AC2237	hypothetical prote
321	27	39.7	293	2	G97555	hypothetical prote	394	27	39.7	532	2	H85035	hypothetical prote

395	27	39.7	537	1	YRH06	lysine-related	468	26	38.2	175	2	AG1984	hypothetical prote
396	27	39.7	551	2	C71606	ATP synthase alpha	469	26	38.2	178	2	H64253	chemotaxis protein
397	27	39.7	558	2	B87098	conserved hypothet	470	26	38.2	181	2	C97709	hypothetical prote
398	27	39.7	558	2	G70879	hypothetical prote	471	26	38.2	181	2	A71713	cdp-diacylglycerol
399	27	39.7	575	2	T24681	hypothetical prote	472	26	38.2	189	2	T23747	hypothetical prote
400	27	39.7	576	2	C88950	protein R09B5.11 (473	26	38.2	191	2	G83161	probable DNA inver
401	27	39.7	585	2	I46686	complement compone	474	26	38.2	197	2	JC3230	hypothetical 22K p
402	27	39.7	586	1	S47452	probable serine/ch	475	26	38.2	199	2	B82315	hypothetical prote
403	27	39.7	588	2	S40925	hypothetical prote	476	26	38.2	200	2	F83008	hypothetical prote
404	27	39.7	607	2	T39823	hypothetical prote	477	26	38.2	216	2	JE0245	Ig lambda chain N1
405	27	39.7	614	2	A12882	MFS permease [suga	478	26	38.2	221	2	F81295	cytochrome-c oxida
406	27	39.7	632	2	AE3560	proline/betaine tr	479	26	38.2	221	2	T46918	hypothetical prote
407	27	39.7	656	2	B84547	hypothetical prote	480	26	38.2	232	1	A64538	cytochrome-c oxida
408	27	39.7	657	2	G97658	hypothetical prote	481	26	38.2	232	2	H71969	cytochrome oxida
409	27	39.7	699	2	P97721	elongation factor	482	26	38.2	236	2	C35620	coenzyme F420 hyd
410	27	39.7	699	2	B71723	translation elonga	483	26	38.2	246	2	F70858	hypothetical prote
411	27	39.7	701	2	S31150	translation elonga	484	26	38.2	247	2	T27778	hypothetical prote
412	27	39.7	701	2	H87143	elongation factor	485	26	38.2	252	2	F70091	hypothetical prote
413	27	39.7	701	2	E70827	probable fusa prot	486	26	38.2	255	2	I38426	lymphocyte activat
414	27	39.7	707	2	JC7763	neuronal leucine-r	487	26	38.2	255	2	E82363	conserved hypothet
415	27	39.7	726	2	T33995	hypothetical prote	488	26	38.2	258	2	A33953	enterotoxin D prec
416	27	39.7	730	2	C69038	transcription regu	489	26	38.2	259	2	T04850	hypothetical prote
417	27	39.7	732	1	S24124	trimethylamine deh	490	26	38.2	261	2	B97589	1-2,3-butanediol d
418	27	39.7	773	2	T27382	hypothetical prote	491	26	38.2	261	2	AG2810	short chain dehydr
419	27	39.7	786	2	S44837	K02D10.1 protein -	492	26	38.2	261	2	A12582	conserved hypothet
420	27	39.7	797	2	T05247	methionine-tRNA 1i	493	26	38.2	261	2	G97364	ATP synthase chain
421	27	39.7	811	2	T04638	hypothetical prote	494	26	38.2	268	2	AG0332	conserved hypothet
422	27	39.7	882	2	AF0306	nitrate reductase	495	26	38.2	271	2	AD0250	conserved hypothet
423	27	39.7	885	2	G95980	probable nitrate r	496	26	38.2	276	2	C72458	hypothetical prote
424	27	39.7	903	2	E98249	nitrate reductase	497	26	38.2	277	2	JQ0927	3A protein - tomat
425	27	39.7	915	2	B48225	probable propenol	498	26	38.2	284	2	S17820	protoporphyrin IX
426	27	39.7	927	2	P82818	conserved hypothet	499	26	38.2	284	2	S76536	hypothetical prote
427	27	39.7	949	2	T16812	hypothetical prote	500	26	38.2	288	2	E83946	pyruvate synthase
428	27	39.7	960	2	T07680	VPS41 protein homo	501	26	38.2	296	2	C87449	phenylalanine-4-hy
429	27	39.7	1063	2	T38420	probable DNA helic	502	26	38.2	294	2	A53372	lysR-type regulato
430	27	39.7	1088	2	B85068	UV-damaged DNA bin	503	26	38.2	298	2	A49630	ubiquitin conjugat
431	27	39.7	1102	2	T04941	UV-damaged DNA-bin	504	26	38.2	299	2	H87567	hypothetical prote
432	27	39.7	1115	2	T09403	integrin alpha cha	505	26	38.2	300	2	F84365	probable isopenten
433	27	39.7	1115	2	T09403	integrin alpha cha	506	26	38.2	301	2	A83017	probable transcrip
434	27	39.7	1139	2	T33275	hypothetical prote	507	26	38.2	303	1	P38VAM	3A protein - brome
435	27	39.7	1217	2	S52714	sericin1B - silkwo	508	26	38.2	307	2	AE3487	hypothetical prote
436	27	39.7	1260	1	TVR2TU	protein-tyrosine k	509	26	38.2	303	2	AE4460	dieneolactone hydro
437	27	39.7	1319	2	S75095	P-glycoprotein - T	510	26	38.2	309	2	B64531	probable lacyl-car
438	27	39.7	1534	2	T30295	hypothetical prote	511	26	38.2	309	2	F71976	probable lacyl-car
439	27	39.7	1557	2	T28811	hypothetical prote	512	26	38.2	311	2	A81179	protein-export mem
440	27	39.7	1603	2	T24098	hypothetical prote	513	26	38.2	312	2	E69753	efflux system homo
441	27	39.7	1927	2	S01168	beta-glycosidase c	514	26	38.2	325	2	E96620	hypothetical prote
442	27	39.7	1928	2	JS0610	beta-galactosidase	515	26	38.2	327	2	H86829	carboxymethylcellu
443	27	39.7	2482	2	I48922	cation-independent	516	26	38.2	327	2	G33282	hypothetical prote
444	27	39.7	2483	1	A49617	insulin-like growt	517	26	38.2	330	2	S60211	DNA ligase homolo
445	27	39.7	2493	1	A30788	mannose 6-phosphat	518	26	38.2	333	2	A75365	2-oxoacid-ferredox
446	27	39.7	2664	2	T28626	variant-specific s	519	26	38.2	335	2	S37304	probable pectinect
447	27	39.7	3078	2	T28432	proline/betaine tr	520	26	38.2	339	2	D87225	hypothetical prote
448	27	39.7	435	2	B97846	glucagon receptor	521	26	38.2	341	2	JC1201	glycoprotein D pre
449	27	39.7	485	2	JC4363	glucagon receptor	522	26	38.2	341	2	A70598	probable regulator
450	26.5	39.0	485	2	J03957	glutamine-tRNA lig	523	26	38.2	345	2	T14707	hypothetical prote
451	26.5	39.0	485	2	T09643	glutamine-tRNA lig	524	26	38.2	348	1	A63194	DNA ligase homolo
452	26.5	39.0	485	2	A43434	luciferin (EC 3.4.21.7	525	26	38.2	352	2	C84603	2-oxoacid-ferredox
453	26	38.2	66	2	G81163	bacterioferritin-a	526	26	38.2	353	2	T04780	probable pectinect
454	26	38.2	70	1	XISR1A	insect toxin 1 - S	527	26	38.2	354	1	VGBE67	hypothetical prote
455	26	38.2	88	2	G34444	insect toxin 2 pre	528	26	38.2	354	2	D70808	glycoprotein D pre
456	26	38.2	101	2	AH2121	hypothetical prote	529	26	38.2	360	2	E96690	hypothetical prote
457	26	38.2	105	2	G72606	hypothetical prote	530	26	38.2	362	2	G87470	hypothetical prote
458	26	38.2	114	2	AE2761	hypothetical prote	531	26	38.2	362	2	C82070	hypothetical prote
459	26	38.2	133	2	C24925	lactose permease -	532	26	38.2	364	2	H71440	conserved hypothet
460	26	38.2	133	2	JH0270	chondromodulin II	533	26	38.2	364	2	E81702	hypothetical prote
461	26	38.2	140	2	A84284	hypothetical prote	534	26	38.2	365	2	T15010	phospholipase D fa
462	26	38.2	144	2	D90089	60S ribosomal prot	535	26	38.2	366	2	S46305	hypothetical prote
463	26	38.2	152	1	G25973	perutussis toxin ch	536	26	38.2	376	2	S63613	dihydrodipicolinat
464	26	38.2	157	2	T20794	hypothetical prote	537	26	38.2	378	2	T46096	probable hsp-bindi
465	26	38.2	167	2	C97542	hypothetical prote	538	26	38.2	378	2	S61992	hypothetical prote
466	26	38.2	169	2	AB2233	hypothetical prote	539	26	38.2	380	2	T23546	hypothetical prote
467	26	38.2	173	2	AB3450	invasion protein b	540	26	38.2	382	2	S36476	E2 protein - human

541	26	38.2	382	2	T09632	614	26	38.2	481	2	G82926	hypothetical prote
542	26	38.2	385	2	T26487	615	26	38.2	483	2	S40128	fascin - African c
543	26	38.2	388	2	T46229	616	26	38.2	484	2	T26190	hypothetical prote
544	26	38.2	389	2	AD1918	617	26	38.2	484	2	T34504	hypothetical prote
545	26	38.2	391	2	H85063	618	26	38.2	484	2	S61870	hypothetical prote
546	26	38.2	393	2	G75503	619	26	38.2	499	2	S19886	viir protein - Str
547	26	38.2	394	2	AG0962	620	26	38.2	500	2	B81250	probable site-spec
548	26	38.2	394	2	D90105	621	26	38.2	503	2	B81690	probable sodium-tr
549	26	38.2	396	1	B65169	622	26	38.2	503	2	C71535	probable NADH (ubi
550	26	38.2	396	2	H86051	623	26	38.2	508	2	S74537	anthranilate synth
551	26	38.2	396	2	P91205	624	26	38.2	516	2	H82973	choline transporte
552	26	38.2	396	2	C87379	625	26	38.2	517	2	T03445	glucose-1-phosphat
553	26	38.2	401	2	E63501	626	26	38.2	518	2	T45765	hypothetical prote
554	26	38.2	403	2	C83422	627	26	38.2	528	2	S35272	dihydrofolate redu
555	26	38.2	404	2	AC2159	628	26	38.2	530	2	A42730	trans-acting posit
556	26	38.2	406	2	G64362	629	26	38.2	533	2	T07894	probable inorganic
557	26	38.2	408	2	AF1599	630	26	38.2	534	2	C84811	phosphate transpor
558	26	38.2	410	2	AB3546	631	26	38.2	535	2	T47629	phosphate transpor
559	26	38.2	415	2	T44436	632	26	38.2	535	2	H75369	conserved hypothet
560	26	38.2	415	2	D85061	633	26	38.2	537	2	T07892	probable inorganic
561	26	38.2	416	2	JT0487	634	26	38.2	537	2	S50344	aspartyllopepsin h
562	26	38.2	416	2	UC2544	635	26	38.2	539	2	JH0263	carboxy-terminal p
563	26	38.2	417	1	GRFC	636	26	38.2	540	2	T44683	probable ABC trans
564	26	38.2	417	2	H85528	637	26	38.2	540	2	A95264	hypothetical prote
565	26	38.2	417	2	D90678	638	26	38.2	540	2	AH3032	transporter, proba
566	26	38.2	418	2	P83986	639	26	38.2	541	2	B87532	acyl CoA dehydroge
567	26	38.2	418	2	C97713	640	26	38.2	541	2	I41124	glucose-1-phosphat
568	26	38.2	418	2	E71716	641	26	38.2	542	2	JQ1005	probable phosphat
569	26	38.2	419	2	AC0792	642	26	38.2	542	2	T01124	ABC transporter, A
570	26	38.2	421	2	E71363	643	26	38.2	542	2	B87373	probable ABC trans
571	26	38.2	425	2	F72315	644	26	38.2	543	2	T19345	probable metabolit
572	26	38.2	428	2	E95854	645	26	38.2	545	1	A31933	cytochrome ccc pre
573	26	38.2	428	2	AH3536	646	26	38.2	545	2	T06264	3-dehydroquinat d
574	26	38.2	429	2	F82961	647	26	38.2	546	2	C91274	probable acyl coen
575	26	38.2	430	2	C42284	648	26	38.2	546	2	C86115	probable acyl coen
576	26	38.2	431	1	ZTEC3	649	26	38.2	550	2	A87252	major facilitator
577	26	38.2	431	1	ZTEC6	650	26	38.2	550	2	AB2000	ATP-binding protei
578	26	38.2	432	2	AB0852	651	26	38.2	555	2	S56946	probable membrane
579	26	38.2	432	2	D85905	652	26	38.2	557	2	D98253	hypothetical prote
580	26	38.2	432	2	JN0080	653	26	38.2	567	2	T14315	dihydrofolate redu
581	26	38.2	432	2	F91060	654	26	38.2	579	2	H87451	exodeoxyribonuclea
582	26	38.2	432	2	A85436	655	26	38.2	581	2	B81107	exodeoxyribonuclea
583	26	38.2	434	2	AF0585	656	26	38.2	581	2	B81909	exodeoxyribonuclea
584	26	38.2	434	2	J00576	657	26	38.2	589	2	T42244	probable polypepti
585	26	38.2	435	2	E82848	658	26	38.2	591	2	G86445	hypothetical prote
586	26	38.2	435	2	H69607	659	26	38.2	592	2	F86242	unknown protein, 9
587	26	38.2	437	2	G97630	660	26	38.2	613	2	JC7992	negatively regulat
588	26	38.2	437	2	AB2854	661	26	38.2	614	2	T29902	hypothetical prote
589	26	38.2	438	2	G90473	662	26	38.2	617	2	F71359	proline-tRNA ligas
590	26	38.2	443	2	JQ1527	663	26	38.2	662	2	T46228	hypothetical prote
591	26	38.2	445	2	S19990	664	26	38.2	666	2	B70803	hypothetical prote
592	26	38.2	447	2	C84306	665	26	38.2	678	2	H71816	probable type II D
593	26	38.2	447	2	B64152	666	26	38.2	698	2	E85369	hypothetical prote
594	26	38.2	449	2	A41738	667	26	38.2	698	2	T10682	hypothetical prote
595	26	38.2	449	2	AB2887	668	26	38.2	702	2	T12624	NADH2 dehydrogen
596	26	38.2	456	2	T06589	669	26	38.2	726	1	C5EC6P	catalase (EC 1.11.
597	26	38.2	458	2	A46366	670	26	38.2	726	2	C86085	catalase, hydrop
598	26	38.2	458	2	T01969	671	26	38.2	726	2	G91237	hydroperoxidase HP
599	26	38.2	458	2	E70145	672	26	38.2	732	2	F91236	primosomal protein
600	26	38.2	459	2	JC6520	673	26	38.2	732	2	F86083	primosomal protein
601	26	38.2	461	2	AE3208	674	26	38.2	732	2	A35505	primosomal replica
602	26	38.2	461	2	H84099	675	26	38.2	747	2	B95363	probable oxidoredu
603	26	38.2	462	2	T15543	676	26	38.2	753	2	T19338	hypothetical prote
604	26	38.2	463	2	A40013	677	26	38.2	754	2	S75113	catalase (EC 1.11.
605	26	38.2	463	2	H82979	678	26	38.2	768	2	S52684	probable membrane
606	26	38.2	467	2	B65020	679	26	38.2	770	2	S00643	anthranilate synth
607	26	38.2	467	2	A91043	680	26	38.2	770	2	S11161	ribochitinase synth
608	26	38.2	467	2	D85887	681	26	38.2	771	1	WMVZ9J	ribochitinase-dip
609	26	38.2	472	2	AE2838	682	26	38.2	771	1	WMVZ9J	ribochitinase-dip
610	26	38.2	472	2	T39615	683	26	38.2	771	2	B36843	ribochitinase-dip
611	26	38.2	475	2	T39359	684	26	38.2	771	2	B36843	ribochitinase-dip
612	26	38.2	476	2	AE1829	685	26	38.2	771	2	H72157	Ldl protein - vari
613	26	38.2	477	2	G97662	686	26	38.2	781	2	P82584	catalase/peroxid

687	26	38.2	800	2	AD3129	conserved hypother	760	25	36.8	111	2	AB2842	conserved hypother
688	26	38.2	808	2	E64914	dimethylsulfoxide	761	25	36.8	114	2	S11952	hypothetical prote
689	26	38.2	808	2	E90915	probable oxidoredu	762	25	36.8	119	1	PSOXA	phospholipase A2 (
690	26	38.2	808	2	B85764	probable oxidoredu	763	25	36.8	126	2	AF2880	hypothetical prote
691	26	38.2	812	2	AB0680	probable dimethyl	764	25	36.8	127	2	B89778	conserved hypother
692	26	38.2	815	2	E98158	hypothetical prote	765	25	36.8	129	2	T20081	hypothetical prote
693	26	38.2	819	2	S43748	translation elonga	766	25	36.8	129	2	T21818	hypothetical prote
694	26	38.2	821	2	B84509	probable Na/H anti	767	25	36.8	131	1	WEBR41	pertussis toxin ch
695	26	38.2	825	2	T00818	hypothetical prote	768	25	36.8	132	1	LZWK	lysosome IEC 3.2.1
696	26	38.2	827	1	S10639	fructose phosphor	769	25	36.8	132	2	G97202	hypothetical prote
697	26	38.2	829	2	S75776	plep protein - syn	770	25	36.8	133	2	T17300	hypothetical prote
698	26	38.2	832	2	B96702	hypothetical prote	771	25	36.8	134	2	AH2645	conserved hypother
699	26	38.2	833	2	T24682	hypothetical prote	772	25	36.8	136	2	A69521	conserved hypother
700	26	38.2	845	2	C82135	chitinase VC1952.1	773	25	36.8	139	2	A38744	lysosome IEC 3.2.1
701	26	38.2	846	2	H70599	hypothetical prote	774	25	36.8	140	2	AE2689	conserved hypother
702	26	38.2	857	2	AC2132	hypothetical prote	775	25	36.8	142	2	H97470	hypothetical prote
703	26	38.2	868	2	AF3204	autotransporter pr	776	25	36.8	145	2	H97427	hypothetical prote
704	26	38.2	890	2	E84846	probable receptor-	777	25	36.8	145	2	H75262	hypothetical prote
705	26	38.2	896	2	G96946	hypothetical prote	778	25	36.8	148	2	S65981	Yyb protein - Bac
706	26	38.2	899	2	G02428	hypothetical prote	779	25	36.8	149	2	B75449	conserved hypother
707	26	38.2	905	2	S56295	SAP155 protein - y	780	25	36.8	150	2	F68714	spore formation pr
708	26	38.2	915	1	A48225	subtilisin-like pr	781	25	36.8	151	2	T38838	hypothetical prote
709	26	38.2	915	1	JC6148	subtilisin-like pr	782	25	36.8	152	1	H25973	pertussis toxin ch
710	26	38.2	964	2	T05382	hypothetical prote	783	25	36.8	155	2	AE2487	hypothetical prote
711	26	38.2	970	2	J00302	hypothetical 112K	784	25	36.8	158	2	F87545	transcription regu
712	26	38.2	985	2	S59330	Na ⁺ /H ⁺ -exchanging	785	25	36.8	160	2	F87307	spu RNA methylas
713	26	38.2	992	2	UQ1165	Env protein - Maed	786	25	36.8	162	2	T49420	hypothetical prote
714	26	38.2	998	2	S77225	Sensory transducti	787	25	36.8	164	2	AB7556	hypothetical prote
715	26	38.2	1013	2	A87304	Tomb-dependent rec	788	25	36.8	165	1	JN0778	ribosomal protein
716	26	38.2	1036	2	T31673	N-acetylglucosamin	789	25	36.8	165	1	R7RT12	ribosomal protein
717	26	38.2	1062	2	B26330	hypothetical prote	790	25	36.8	165	2	S35531	ribosomal protein
718	26	38.2	1103	2	A85189	disease resistance	791	25	36.8	165	2	T23150	hypothetical prote
719	26	38.2	1170	2	A53612	laminin BLK chain	792	25	36.8	167	2	E83034	urease accessory p
720	26	38.2	1204	2	S62506	alpha-glucan synth	793	25	36.8	169	2	S60891	hypothetical prote
721	26	38.2	1234	2	B36186	I factor protein 2	794	25	36.8	171	2	G70636	hypothetical prote
722	26	38.2	1371	2	H82024	probable periplasm	795	25	36.8	174	2	G81823	hypothetical prote
723	26	38.2	1402	2	S62557	probable calcium-t	796	25	36.8	174	2	B95940	hypothetical prote
724	26	38.2	1405	1	A48196	protein-tyrosine k	797	25	36.8	178	1	RSRT11	ribosomal protein
725	26	38.2	1405	2	H81003	conserved hypother	798	25	36.8	178	2	D68265	hist protein - Zym
726	26	38.2	1445	2	A59437	KIAA1204 protein (799	25	36.8	179	2	D98265	hypothetical prote
727	26	38.2	1548	2	S34583	serine proteinase	800	25	36.8	183	2	AE3019	conserved hypother
728	26	38.2	1662	2	T18540	mofa protein precu	801	25	36.8	184	2	S60245	ribosomal protein
729	26	38.2	1713	2	A55347	adhesive ligand ep	802	25	36.8	184	2	A82446	hypothetical prote
730	26	38.2	1745	2	S44816	P4AE2.1 protein -	803	25	36.8	185	2	D84538	probable glycine-r
731	26	38.2	1887	2	S61703	faty-acid synthas	804	25	36.8	186	1	DEPSNL	amine dehydrogenas
732	26	38.2	2265	1	FNEO	fibronectin - bov1	805	25	36.8	186	2	G81093	amine dehydrogenas
733	26	38.2	2272	2	T18572	gag, pol and env p	806	25	36.8	186	2	H81846	hypothetical lipop
734	26	38.2	2386	1	FNHU	genome polyprotein	807	25	36.8	187	2	T10073	amine dehydrogenas
735	26	38.2	2412	1	J01537	probable resistant	808	25	36.8	188	1	JH0661	amine dehydrogenas
736	26	38.2	2467	2	D71437	Xotch protein - Af	809	25	36.8	188	2	G75326	amine dehydrogenas
737	26	38.2	2524	2	A35844	phosphotidylinosit	810	25	36.8	188	2	G75326	probable 16S rRNA
738	26	38.2	2812	2	T43271	hypothetical prote	811	25	36.8	191	2	F96803	hypothetical prote
739	26	38.2	2957	2	T33152	hypothetical prote	812	25	36.8	196	2	T29860	hypothetical prote
740	26	38.2	3712	2	S18253	laminin alpha-1 ch	813	25	36.8	196	2	T30978	protein C26E6.1 [1
741	26	38.2	5327	2	T13564	microtubule-associ	814	25	36.8	196	2	H88445	conserved hypother
742	26	38.2	8563	2	T30226	polyketide synthas	815	25	36.8	198	2	AB3182	hypothetical prote
743	25.5	37.5	125	2	T16247	hypothetical prote	816	25	36.8	201	2	F72390	probable lipoprote
744	25.5	37.5	231	2	S25753	Ig lambda chain -	817	25	36.8	202	2	H70760	proteasome endopep
745	25.5	37.5	341	2	S09913	hypothetical prote	818	25	36.8	204	2	T51981	hypothetical prote
746	25.5	37.5	406	2	T23898	hypothetical prote	819	25	36.8	204	2	F86350	hypothetical prote
747	25.5	37.5	428	2	AB3494	hypothetical prote	820	25	36.8	207	2	T20391	hypothetical prote
748	25.5	37.5	430	2	T23899	hypothetical prote	821	25	36.8	209	2	T19025	hypothetical prote
749	25.5	37.5	630	2	A49656	estrogen-responsiv	822	25	36.8	212	2	G75359	conserved hypother
750	25.5	37.5	1079	2	F82447	pyruvate-flavoredo	823	25	36.8	213	2	S72625	hypothetical prote
751	25	36.8	40	2	B31791	sarcotoxin ID - fl	824	25	36.8	214	2	I40768	probable lipoprote
752	25	36.8	60	2	S68769	shot neurotoxin -	825	25	36.8	215	2	S74854	hypothetical prote
753	25	36.8	68	2	AD2576	nifu protein - Nos	826	25	36.8	215	2	AB3358	deoxyribose-phosph
754	25	36.8	75	2	B28186	ribosomal protein	827	25	36.8	219	2	A70314	conjugal transfer
755	25	36.8	79	2	S07562	hypothetical prote	828	25	36.8	220	2	T00654	hypothetical prote
756	25	36.8	79	2	AC2103	probable integral	829	25	36.8	222	2	T16335	hypothetical prote
757	25	36.8	111	2	D81780	multidrug resistan	830	25	36.8	223	2	E75390	phase shock protei
758	25	36.8	111	2	A81204	hypothetical prote	831	25	36.8	223	2	T05755	hypothetical prote
759	25	36.8	111	2	C97619	hypothetical prote	832	25	36.8	223	2		

833	25	36.8	224	2	T16705	hypothetical prote	906	25	36.8	316	2	C81097	thioredoxin reduct
834	25	36.8	226	2	S76020	endopeptidase Clp	907	25	36.8	316	2	E81845	thioredoxin-disulf
835	25	36.8	226	2	AD3282	phosphate regulon	908	25	36.8	316	2	E81845	acidic ribosomal p
836	25	36.8	227	2	E75066	probable translati	909	25	36.8	316	2	E50151	hypothetical prote
837	25	36.8	227	2	D71166	hypothetical prote	910	25	36.8	319	2	B64304	hypothetical prote
838	25	36.8	242	2	S62017	phenylacrylic acid	911	25	36.8	320	2	G84241	hypothetical prote
839	25	36.8	242	2	F30315	methyl viologen-re	912	25	36.8	320	2	S69547	transcription init
840	25	36.8	242	2	AC0131	probable copper ho	913	25	36.8	320	2	S38670	chitinase (EC 3.2.
841	25	36.8	243	2	S42533	uroporphyrinogen I	914	25	36.8	320	2	AE2588	mutr/nudix family
842	25	36.8	244	2	AC2751	transcription regul	915	25	36.8	322	2	B97370	NADH pyrophosphat
843	25	36.8	244	2	C97532	probable transcrip	916	25	36.8	322	2	G97396	cysteine synthase
844	25	36.8	247	2	T28865	hypothetical prote	917	25	36.8	324	2	B97298	cytochrome-c3 hyd
845	25	36.8	248	2	B72240	deoxyribose-phosph	918	25	36.8	327	2	B95960	characterized Fe-
846	25	36.8	248	2	D69073	nitrate assimilati	919	25	36.8	327	2	AC2779	probable cytochrom
847	25	36.8	251	2	T42005	conserved hypothet	920	25	36.8	327	2	G97558	hypothetical prote
848	25	36.8	252	1	JN0392	matrix protein M1	921	25	36.8	327	2	G96833	hypothetical prote
849	25	36.8	252	1	MFIV	matrix protein M1	922	25	36.8	328	2	S42593	hypothetical prote
850	25	36.8	252	1	MFIV1K	matrix protein M1	923	25	36.8	330	2	D70348	ADP-ribosylglycohy
851	25	36.8	252	1	PN0086	matrix protein M1	924	25	36.8	330	2	A87662	conserved hypothet
852	25	36.8	252	1	B45539	matrix protein M1	925	25	36.8	332	2	B81665	proteinase IV, pro
853	25	36.8	252	1	MFIVM	matrix protein M1	926	25	36.8	332	2	G83270	beta-N-acetyl-D-gl
854	25	36.8	252	1	MFIVM1	matrix protein M1	927	25	36.8	334	2	B85775	hypothetical prote
855	25	36.8	252	1	MFIVC	matrix protein M1	928	25	36.8	334	2	A99927	hypothetical prote
856	25	36.8	252	1	MFIVMS	matrix protein M1	929	25	36.8	335	2	F64925	ynbg protein - Bac
857	25	36.8	252	1	PN0083	matrix protein M1	930	25	36.8	335	2	T52577	glibetreltin 2beta-
858	25	36.8	252	2	S04058	matrix protein M1	931	25	36.8	335	2	B45511	chitinase (EC 3.2.
859	25	36.8	252	2	S04050	matrix protein M1	932	25	36.8	336	2	T20854	hypothetical prote
860	25	36.8	252	2	T09279	matrix protein M1	933	25	36.8	336	2	H82615	3-oxoacyl-[ACP] sy
861	25	36.8	252	2	S04056	matrix protein M1	934	25	36.8	339	1	RRVOBM	RNA-directed RNA p
862	25	36.8	252	2	S04052	matrix protein M1	935	25	36.8	339	1	RRVOBM	RNA-directed RNA p
863	25	36.8	252	2	S14616	matrix protein M1	936	25	36.8	340	2	S69194	N4-(beta-N-acetyl)g
864	25	36.8	252	2	S07429	matrix protein M1	937	25	36.8	341	2	I61725	natural killer ass
865	25	36.8	252	2	S04054	matrix protein M1	938	25	36.8	341	2	T16091	hypothetical prote
866	25	36.8	256	2	E95912	probable acetyltra	939	25	36.8	342	1	T24660	probable phosphos
867	25	36.8	258	2	G65054	hypothetical prote	940	25	36.8	343	1	JC7958	galaxin precursor
868	25	36.8	260	2	AG2658	conserved hypothet	941	25	36.8	344	2	T19367	cytochrome-c3 hyd
869	25	36.8	262	2	B53422	peptidylprolyl iso	942	25	36.8	346	2	H84751	hypothetical prote
870	25	36.8	264	2	AE2274	hypothetical prote	943	25	36.8	346	2	T51424	probable peroxidase
871	25	36.8	265	2	DE4198	endonuclease III l	944	25	36.8	348	2	G86985	hypothetical prote
872	25	36.8	265	2	T26217	hypothetical prote	945	25	36.8	348	2	A56247	probable sulphate-
873	25	36.8	267	2	E81431	ABC transporter in	946	25	36.8	354	2	T23655	natural killer cel
874	25	36.8	269	2	B69461	hypothetical prote	947	25	36.8	355	2	P00207	hypothetical prote
875	25	36.8	269	2	G69845	enoyl-l-acyl-carrie	948	25	36.8	358	2	S72585	protein kinase (BC
876	25	36.8	275	2	D97440	ATP synthase (Atp1	949	25	36.8	358	2	T03305	sulfate-binding pr
877	25	36.8	278	2	A83689	hypothetical prote	950	25	36.8	358	2	H84496	probable 3'-(2')-5'
878	25	36.8	279	1	P3VXV1	3a protein - cucum	951	25	36.8	359	2	T03214	probable retroelem
879	25	36.8	279	1	C71392	movement protein -	952	25	36.8	359	2	T52383	dihydrodipicolinat
880	25	36.8	279	2	J50089	3A protein - cucum	953	25	36.8	360	2	G72235	hypothetical prote
881	25	36.8	281	2	E71046	probable ferredoxi	954	25	36.8	365	2	B84890	probable dihydrodi
882	25	36.8	281	2	G75168	2-ketoglutarate fe	955	25	36.8	365	2	H84471	hypothetical prote
883	25	36.8	283	2	G87554	transcription regul	956	25	36.8	365	2	E97315	membrane protease
884	25	36.8	286	2	T26657	hypothetical prote	957	25	36.8	367	2	S48833	cytochrome-c3 hyd
885	25	36.8	288	2	T38075	conserved hypothet	958	25	36.8	367	2	E75133	cytochrome-c3 hyd
886	25	36.8	292	2	F97774	hypothetical prote	959	25	36.8	372	2	AH0667	conserved hypothet
887	25	36.8	293	2	S46710	hypothetical prote	960	25	36.8	372	2	JC2556	alpha-1-microglobu
888	25	36.8	295	2	S60711	band-6-protein - b	961	25	36.8	372	2	G71074	probable cytochrom
889	25	36.8	298	2	C82824	cell division inhi	962	25	36.8	374	2	E90292	transport membrane
890	25	36.8	299	2	E75254	conserved hypothet	963	25	36.8	374	2	AH3522	xylose repressor l
891	25	36.8	300	1	D34443	nitrogen fixation	964	25	36.8	375	2	D97268	toxic anion resist
892	25	36.8	300	2	AD1988	nitrogen fixation	965	25	36.8	377	1	WZWT6	dihydrodipicolinat
893	25	36.8	300	2	AF3098	conserved hypothet	966	25	36.8	378	2	AG2833	hypothetical prote
894	25	36.8	300	2	D98194	hypothetical prote	967	25	36.8	378	2	C97611	hypothetical prote
895	25	36.8	307	2	A27389	catechol 2,3-dioxy	968	25	36.8	379	2	H83727	phosphoribosylam
896	25	36.8	308	2	T15055	dihydrodipicolinat	969	25	36.8	380	1	WZMP	phosphoribosylam
897	25	36.8	308	2	T44614	cysteine synthase	970	25	36.8	382	2	S08595	Ttfa transcription
898	25	36.8	308	2	AF0809	probable transcrip	971	25	36.8	383	2	G55244	hypothetical 41.7
899	25	36.8	308	2	B69329	hypothetical prote	972	25	36.8	384	2	G84650	probable beta-gluc
900	25	36.8	308	2	AC1053	probable membrane	973	25	36.8	384	2	G84850	hypothetical prote
901	25	36.8	309	2	T02304	2'-hydroxyisoflavo	974	25	36.8	386	2	A10937	cystathionine gamm
902	25	36.8	312	2	AB1350	3-oxoacyl- acyl-ca	975	25	36.8	386	2	G64494	quinolone resistan
903	25	36.8	312	2	AB1720	3-oxoacyl- acyl-ca	976	25	36.8	387	2	A10511	probable metabolit
904	25	36.8	313	2	T26308	hypothetical prote	977	25	36.8	388	1	WZWT7	dihydrodipicolinat
905	25	36.8	313	2	S61990	hypothetical prote	978	25	36.8	388	2	D84952	tryptophan synthas

979 25 36.8 388 2 C71961 succinyl-diaminopip
980 25 36.8 388 2 AC2011 hypotetical prote
981 25 36.8 389 2 C82987 probable MFS trans
982 25 36.8 393 2 S27881 beta-alanine synth
983 25 36.8 393 2 F72594 cystathionine beta
984 25 36.8 394 2 F86190 hypotetical prote
985 25 36.8 394 2 F82507 proteinase Vch0045
986 25 36.8 395 2 G70633 probable fader7 pro
987 25 36.8 396 1 XNECD aspartate transam
988 25 36.8 396 2 AD0616 aspartate aminotra
989 25 36.8 396 2 A85619 aspartate aminotra
990 25 36.8 396 2 C90755 aspartate aminotra
991 25 36.8 396 2 I64132 aspartate transam
992 25 36.8 396 2 AD0172 aspartate transam
993 25 36.8 397 1 PC1219 dihydroorotate oxi
994 25 36.8 397 2 C81188 aspartate transam
995 25 36.8 397 2 B81915 aspartate transam
996 25 36.8 397 2 F96680 F514.10 [imported
997 25 36.8 397 2 G69295 oxalate/formate an
998 25 36.8 398 2 T35982 probable peptide t
999 25 36.8 399 2 AH2542 hypotetical prote
1000 25 36.8 401 2 S65044 phosphoglycerate k

ALIGNMENTS

RESULT 1
S01657
atrial natriuretic factor - laughing frog (tentative sequence) (fragment)

N/Alternate names: atropoepin
C/Species: Rana ridibunda (laughing frog)
C/Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C/Accession: S01657; A20977
R/Author: C.; Ong, H.; McNicol, N.; Netchitailo, P.; Chretien, M.; de Lean, A.; Vaudry, P.
P/RS Lett: 238, 300-306, 1988
A/Title: The amino acid sequences of frog heart atrial natriuretic-like peptide and mamm
A/Reference number: S01657; MUID:89005705; PMID:2971573
A/Molecule type: protein
A/Residues: 1-30 <LAZ>
A/Accession: S01657
A/Cross-references: UNIPROT:P09196; UNIPARC:UPI00000351P2
A/Note: the sequence from the summary is inconsistent with that from Fig. 3 in lacking
C/Superfamily: natriuretic peptide A precursor

Query Match 82.4%; Score 56; DB 2; Length 30;
Best Local Similarity 58.8%; Pred. No. 2.5e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
DB 11 CFGSRIDRIGAGSGMGC 27

RESULT 2
S14872
atrial natriuretic peptide precursor - guinea pig (fragment)
C/Species: Cavia porcellus (guinea pig)
C/Date: 20-Feb-1995 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004
C/Accession: S14872
R/Author: H. J.; Hanke, M.; Schmieding, G.; Teuteberg, K.; Schulz-Knappe, P.; Forssmann, R.
Submitted to the EMBL Data Library, March 1991
A/Reference number: S14872
A/Accession: S14872
A/Molecule type: mRNA
A/Residues: 1-128 <MAE>
A/Cross-references: UNIPROT:P27596; UNIPARC:UPI0000125AF9; EMBL:X58562; NID:G49543; P1DN
A/Superfamily: natriuretic peptide A precursor
A/Experimental source: heart atria; adult
C/Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation
F/1-96/Domain: signal sequence #status predicted <Sig>
F/99-128/Product: atrial natriuretic peptide #status predicted <Mat>
F/105-121/Disulfide bonds: #status predicted

Query Match 82.4%; Score 56; DB 2; Length 128;
Best Local Similarity 58.8%; Pred. No. 9.2e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
DB 105 CFGSRMDRIGAGSSILGC 121

RESULT 3

J00947
atrial natriuretic peptide precursor - bullfrog

N/Alternate names: ANP; atrial natriuretic factor (ANF)
C/Species: atrial natriuretic peptide-21; atrial natriuretic peptide-24
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: J00947; A31510
R/Kojima, M.
Submitted to JRPID, May 1991
A/Reference number: J00947
A/Accession: J00947
A/Molecule type: mRNA
A/Residues: 1-145 <KOU>
A/Cross-references: UNIPROT:P18909; UNIPARC:UPI0000125AF9
R/Sakata, J.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 155, 1338-1345, 1988
A/Title: Identification of new atrial natriuretic peptides in frog heart.
A/Reference number: A31510; MUID:89025806; PMID:2972279
A/Accession: A31510
A/Molecule type: protein
A/Residues: 122-145 <SAK>
A/Cross-references: UNIPARC:UPI00000351EP
C/Comment: In mammals, several active peptides may be derived from the prohormone.
C/Superfamily: natriuretic peptide A precursor
C/Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation
F/1-23/Domain: signal sequence #status predicted <PRO>
F/24-121/Domain: propeptide #status predicted <PRO>
F/122-145/Product: atrial natriuretic peptide-24 #status experimental <M24>
F/125-145/Product: atrial natriuretic peptide-21 #status experimental <M21>
F/125-141/Disulfide bonds: #status predicted

Query Match 82.4%; Score 56; DB 1; Length 145;
Best Local Similarity 58.8%; Pred. No. 0.0001;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
DB 125 CFGSRIDRIGAGSGMGC 141

RESULT 4

JT0581
natriuretic peptide type C - chicken

C/Species: Gallus gallus (chicken)
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C/Accession: JT0581
R/Author: J. J.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 174, 142-148, 1991
A/Title: Isolation and identification of C-type natriuretic peptide in chicken brain.
A/Reference number: JT0581; MUID:91113186; PMID:1989595
A/Accession: JT0581
A/Molecule type: protein
A/Residues: 1-22 <ARI>
A/Cross-references: UNIPROT:P21805; UNIPARC:UPI0000035211
A/Experimental source: brain
C/Superfamily: natriuretic peptide A precursor
C/Keywords: diuretic; hormone; natriuretic; osmoregulation

Query Match 80.9%; Score 55; DB 2; Length 22;
Best Local Similarity 58.8%; Pred. No. 3.1e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;


```
A:Reference number: S71379; MUID:96354866; PMID:8769304
A:Accession: S71381
A:Molecule type: protein
A:Residues: 1-38 <BAR>
A:Cross-references: UNIPROT:Q7L209; UNIPARC:UPI0000030733
A:Experimental source: venom
A:Accession: S71382
A:Molecule type: protein
A:Residues: 2-38 <BA2>
A:Cross-references: UNIPARC:UPI0000030734
A:Experimental source: venom
A:Accession: S71379
A:Molecule type: protein
A:Residues: 1-13 <BA3>
A:Cross-references: UNIPARC:UPI000003072F
A:Experimental source: venom
C:Keywords: anticoagulant; venom
P:14-30/Dissulfide bonds: #status predicted

Query Match      80.9%; Score 55; DB 2; Length 38;
Best Local Similarity 58.8%; Pred. No. 5.1e-05;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXGC 17
DB      14 CFGHKIDRIGSHGLGC 30

RESULT 11
A41403
aldosterone secretion inhibitory factor precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: A41403; A30976
R:Nguyen, T.T.; Lazure, C.; Babinaki, K.; Chretien, M.; De Lean, A.; Ong, H.
Mol. Endocrinol. 3, 1823-1829, 1989
A>Title: Purification and primary structure of pro-aldosterone secretion inhibitory fact
A:Reference number: A41403; MUID:90114187; PMID:2532709
A:Accession: A41403
A:Molecule type: protein
A:Residues: 1-103 <NGU>
A:Cross-references: UNIPROT:P13204; UNIPARC:UPI0000125AD9
R:Nguyen, T.T.; Lazure, C.; Babinaki, K.; Chretien, M.; Ong, H.; de Lean, A.
Endocrinology 124, 1591-1593, 1989
A>Title: Aldosterone secretion inhibitory factor: a novel neuropeptide in bovine chromaf
A:Reference number: A30976; MUID:89136947; PMID:2537187
A:Accession: A30976
A:Molecule type: protein
A:Residues: 69-103 <NG2>
A:Cross-references: UNIPARC:UPI0000176580
A:Superfamily: natriuretic peptide A precursor

Query Match      80.9%; Score 55; DB 2; Length 103;
Best Local Similarity 58.8%; Pred. No. 0.00012;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXGC 17
DB      81 CFGRRLDRIIGSLGLGC 97

RESULT 12
B36736
brain natriuretic peptide - dog
C:Species: Canis lupus familiaris (dog)
C>Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 09-Jul-2004
C:Accession: B36736
R:Seilhamer, J.O.; Arfsten, A.; Miller, J.A.; Lundquist, P.; Scarborough, R.M.; Lewicki,
Biochem. Biophys. Res. Commun. 165, 650-658, 1989
A>Title: Human and canine gene homologs of porcine brain natriuretic peptide.
A:Reference number: A36736; MUID:90088474; PMID:2597152
A:Accession: B36736
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-105 <SEI>
A:Cross-references: UNIPROT:P16859; UNIPARC:UPI0000176581; GB:M31777
C:Superfamily: natriuretic peptide A precursor

Query Match      80.9%; Score 55; DB 2; Length 105;
Best Local Similarity 58.8%; Pred. No. 0.00013;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXGC 17
DB      83 CFGRLDRIIGSLGLGC 99

RESULT 13
S15822
natriuretic peptide type C - smaller spotted catshark
C:Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S15822
R:Suzuki, R.; Takahashi, A.; Hazon, N.; Takei, Y.
FBS Lett. 282, 321-325, 1991
A>Title: Isolation of high-molecular-weight C-type natriuretic peptide from the heart of
A:Reference number: S15822; MUID:91243822; PMID:1828036
A:Accession: S15822
A:Molecule type: protein
A:Residues: 1-115 <FEB>
A:Cross-references: UNIPROT:P23259; UNIPARC:UPI0000125AE3
C:Superfamily: natriuretic peptide A precursor

Query Match      80.9%; Score 55; DB 1; Length 115;
Best Local Similarity 58.8%; Pred. No. 0.00014;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXGC 17
DB      99 CFGVLDRIIGAMSLGLGC 115

RESULT 14
B54119
C-type natriuretic peptide II precursor - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C>Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C:Accession: B54119
R:Kojima, M.; Ohyama, Y.; Miyamoto, K.; Minamino, N.; Kangawa, K.; Matsuo, H.
J. Biol. Chem. 269, 13136-13140, 1994
A>Title: Cloning and characterization of a novel natriuretic peptide in frog (Rana cates
A:Reference number: A54119; MUID:94230409; PMID:8175740
A:Accession: B54119
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-118 <KOU>
A:Cross-references: UNIPROT:P40756; UNIPARC:UPI0000125AE4; GB:D17414; MTD:9397835; PIDN
A>Note: authors translated the codon AAA for residue 89 as Ile
C:Superfamily: natriuretic peptide C precursor

Query Match      80.9%; Score 55; DB 2; Length 118;
Best Local Similarity 58.8%; Pred. No. 0.00014;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CFGXXXDRIGXXSXGC 17
DB      102 CFGKLDRIIGAMSLGLGC 118

RESULT 15
A30162
brain natriuretic factor precursor - rat
N:Alternate names: brain natriuretic peptide; cardiac natriuretic factor; iso-atrial nat
N:Contains: brain natriuretic factor BNP-45
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
```

C:Accession: A30162; A55691; A54893; A32918; A32919; A33253; A60735; I57704; A33252
 R:Ojima, M.; Minamino, N.; Kangawa, K.; Matsuo, H.
 Biochem. Biophys. Res. Commun. 159, 1420-1426, 1989
 A>Title: Cloning and sequence analysis of cDNA encoding a precursor for rat brain natriuretic peptide
 A:Reference number: A30162; MUID:89193742; PMID:2522776
 A:Accession: A30162
 A:Molecule type: mRNA
 A:Residues: 1-121 <KQJ>
 A:Cross-references: UNIPROT:P13205; UNIPARC:UPI0000125ADC; GB:M25297; NID:g602483; PIDN:R:Roy, R.N.; Flynn, T.G.
 Biochem. Biophys. Res. Commun. 171, 416-423, 1990
 A>Title: Organization of the gene for iso-rANP, a rat B-type natriuretic peptide.
 A:Reference number: A35691; MUID:90365739; PMID:2144113
 A:Accession: A35691
 A:Molecule type: DNA
 A:Residues: 1-14, 'V', 16-121 <ROY>
 A:Cross-references: UNIPARC:UPI0000170906; GB:M60731; NID:g204985; PIDN:AAA1456.1; PID:A:Note: the authors translated the codon GGT for residue 15 as Leu
 R:Thuermer, D.J.; Hanford, D.S.; Glembocki, C.C.
 J. Biol. Chem. 269, 17772-17775, 1994
 A>Title: Regulation of rat brain natriuretic peptide transcription. A potential role for
 A:Reference number: A54893; MUID:94289479; PMID:8027030
 A:Accession: A54893
 A:Molecule type: DNA
 A:Residues: 1-19 <THU>
 A:Cross-references: UNIPARC:UPI000000516; GB:U02972; NID:g458021; PIDN:AAA21648.1; PID:R:Aburaya, M.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.
 Biochem. Biophys. Res. Commun. 163, 226-232, 1989
 A>Title: Isolation and identification of rat brain natriuretic peptides in cardiac atria
 A:Reference number: A32918; MUID:89374230; PMID:2673336
 A:Accession: A32918
 A:Molecule type: protein
 A:Residues: 27-121 <ABU>
 A:Cross-references: UNIPARC:UPI00001733AC
 R:Kamabayashi, Y.; Nakao, K.; Itoh, H.; Hosoda, K.; Saito, Y.; Yamada, T.; Mukoyama, M.; Imura, H.
 Biochem. Biophys. Res. Commun. 163, 233-240, 1989
 A>Title: Isolation and sequence determination of rat cardiac natriuretic peptide.
 A:Reference number: A32919; MUID:89374231; PMID:2528349
 A:Accession: A32919
 A:Molecule type: protein
 A:Residues: 77-121 <KAM>
 A:Cross-references: UNIPARC:UPI000003520F
 R:Flynn, T.G.; Brar, A.; Tremblay, L.; Sarda, I.; Lyons, C.; Jennings, D.B.
 Biochem. Biophys. Res. Commun. 161, 830-837, 1989
 A>Title: Isolation and characterization of iso-rANP, a new natriuretic peptide from rat
 A:Reference number: A33253; MUID:89286593; PMID:2525380
 A:Accession: A33253
 A:Molecule type: protein
 A:Residues: 77-119, 'Q', 121 <FLY>
 A:Cross-references: UNIPARC:UPI00001733AD
 R:Nakao, K.; Itoh, H.; Kamabayashi, Y.; Hosoda, K.; Saito, Y.; Yamada, T.; Mukoyama, M.; Hyperextension 15, 774-778, 1990
 A>Title: Rat brain natriuretic peptide. Isolation from rat heart and tissue distribution
 A:Reference number: A60735; MUID:90277148; PMID:2351330
 A:Accession: A60735
 A:Molecule type: protein
 A:Residues: 77-121 <NAK>
 A:Cross-references: UNIPARC:UPI000003520F
 R:Daigino, L.; Drouin, J.; Nemer, M.
 Mol. Endocrinol. 5, 1292-1300, 1991
 A>Title: Differential expression of natriuretic peptide genes in cardiac and extracardiac
 A:Reference number: I57704; MUID:92123224; PMID:1837590
 A:Accession: I57704
 A:Molecule type: DNA
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Residues: 1-121 <RES>
 A:Cross-references: UNIPARC:UPI0000125ADC; GB:M60266; NID:g204983; PIDN:AAA1455.1; PID:C:Genetics:
 A:introns: 42/3; 117/1
 C:Superfamily: natriuretic peptide A precursor
 C:Keywords: cardiac muscle; heart
 F:1-26/Domain: signal sequence #status predicted <SIG>

F:27-121/Product: brain natriuretic factor #status experimental <MAT1>
 F:77-121/Product: brain natriuretic factor BNP-45 #status experimental <MAT2>

Query Match 80.9%; Score 55; DB 1; Length 121;
 Best Local Similarity 58.8%; Pred. No. 0.00014;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CPGXXXDRIGXXSXXGC 17
 DB 99 CPGXKIDRIGAVSRLLGC 115

RESULT 16

A9144
 type-B natriuretic peptide, BNP - mouse

C:Species: Mus musculus (house mouse)
 C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999

C:Accession: A49144
 R:Steinhelper, M.E.

Circ. Res. 72, 984-992, 1993

A>Title: Structure, expression, and genomic mapping of the mouse natriuretic peptide
 A:Reference number: A49144; MUID:93238395; PMID:8097440

A:Accession: A49144
 A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-121 <STE>
 A:Cross-references: UNIPARC:UPI0000176583; GB:S58667; NID:g299794; PIDN:AA26344.1; PID:A:Experimental source: BALB/c

A:Note: sequence inconsistent with the nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBIN:130161, NCBI:130162)

C:Superfamily: natriuretic peptide A precursor

Query Match 80.9%; Score 55; DB 2; Length 121;
 Best Local Similarity 58.8%; Pred. No. 0.00014;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CPGXXXDRIGXXSXXGC 17
 DB 99 CPGXKIDRIGAVSRLLGC 115

RESULT 17

I49548
 brain natriuretic peptide - mouse

C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I49548
 R:Ogawa, Y.; Itoh, H.; Tamura, N.; Suga, S.; Yoshimasa, T.; Uehira, M.; Matsuda, S.; Si

J. Clin. Invest. 93, 1911-1921, 1994
 A>Title: Molecular cloning of the complementary DNA and gene that encode mouse brain n.

A:Reference number: I49548; MUID:94237953; PMID:8182124

A:Accession: I49548
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-121 <RES>

A:Cross-references: UNIPROT:P40753; UNIPARC:UPI0000000CE3; GB:D16497; NID:g493659; PIDN:A:Gene: BNP

A:introns: 42/3; 117/1
 C:Superfamily: natriuretic peptide A precursor

Query Match 80.9%; Score 55; DB 2; Length 121;
 Best Local Similarity 58.8%; Pred. No. 0.00014;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CPGXXXDRIGXXSXXGC 17
 DB 99 CPGXKIDRIGAVSRLLGC 115

RESULT 18

A36155
 natriuretic peptide C precursor - pig

C.Species: Sus scrofa domestica (domestic pig)
 C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C.Accession: A36155; A55423; A34642
 R.Tawarayagi, Y.; Fuchimura, K.; Nakamoto, H.; Tanaka, S.; Minamino, N.; Kangawa, K.; Matsuo, H.
 Biochem. Biophys. Res. Commun. 172, 627-632, 1990
 A.Title: Gene and precursor structure of porcine C-type natriuretic peptide.
 A.Reference number: A36155; MUID:91054445; PMID:2146557
 A.Accession: A36155
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-126 <TAW>
 A.Cross-references: UNIPROT:P18104; UNIPARC:UPI0000125AB0; EMBL:M64758; NID:G309789; PID
 R.Minamino, N.; Kangawa, K.; Matsuo, H.
 Biochem. Biophys. Res. Commun. 170, 973-979, 1990
 A.Title: N-terminally extended form of C-type natriuretic peptide (CNP-53) identified in
 A.Reference number: A35423; MUID:90343827; PMID:2383278
 A.Accession: A35423
 A.Status: preliminary
 A.Molecule type: protein
 A.Residues: 74-126 <MIN>
 A.Cross-references: UNIPARC:UPI0000035212
 R.Sudoh, T.; Minamino, N.; Kangawa, K.; Matsuo, H.
 Biochem. Biophys. Res. Commun. 168, 863-870, 1990
 A.Title: C-type natriuretic peptide (CNP): a new member of natriuretic peptide family id
 A.Reference number: A34642; MUID:90241265; PMID:2139780
 A.Accession: A34642
 A.Status: preliminary
 A.Molecule type: protein
 A.Residues: 105-126 <SUD>
 A.Cross-references: UNIPARC:UPI0000033C90
 C.Superfamily: natriuretic peptide C precursor
 C.Keywords: disulfide bond; diuretic; hormone; natriuretic; osmoregulation
 F.1-23/Domain: signal sequence #status predicted <SIG>
 F.74-126/Product: natriuretic peptide C-53 #status experimental <CS3>
 F.98-126/Product: natriuretic peptide C-29 #status predicted <C29>
 F.105-126/Product: natriuretic peptide C-22 #status experimental <C22>
 F.110-126/Disulfide bonds: #status predicted

Query Match 80.9%; Score 55; DB 1; Length 126;
 Best Local Similarity 58.8%; Pred. No. 0.00015;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
 DB 110 CFGKLKDRIGSMGSLGC 126

RESULT 19

AMHUC
 natriuretic peptide C precursor [validated] - human
 N.Alternate names: natriuretic factor C
 N.Contains: natriuretic peptide C-22; natriuretic peptide C-29; natriuretic peptide C-53
 C.Species: Homo sapiens (man)
 C.Date: 17-Apr-1993 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
 C.Accession: J10567; J10567; J10567; J10567; J10567
 R.Tawarayagi, Y.; Fuchimura, K.; Tanaka, S.; Minamino, N.; Kangawa, K.; Matsuo, H.
 Biochem. Biophys. Res. Commun. 175, 645-651, 1991
 A.Title: Gene and precursor structures of human C-type natriuretic peptide.
 A.Reference number: J10567; MUID:91207363; PMID:2018508
 A.Accession: J10567
 A.Molecule type: DNA
 A.Residues: 1-126 <TAW>
 A.Cross-references: UNIPROT:P23582; UNIPARC:UPI0000033C91; GB:M64710; NID:G180676; PIDN:
 R.Ishizaka, Y.; Kangawa, K.; Minamino, N.; Ishii, K.; Takano, S.; Eto, T.; Matsuo, H.
 Biochem. Biophys. Res. Commun. 189, 697-704, 1992
 A.Title: Isolation and identification of C-type natriuretic peptide in human monocyte
 A.Reference number: J10361; MUID:93112033; PMID:1472040
 A.Accession: J10361
 A.Molecule type: protein
 A.Residues: 98-109 'X', 111-118 <ISH>
 A.Cross-references: UNIPARC:UPI00001733AB
 R.Ogawa, Y.; Nakao, K.; Nakagawa, O.; Komatsu, Y.; Hosoda, K.; Suga, S.; Arai, H.; Nagat
 Hypertension 19, 809-813, 1992

A.Title: Human C-type natriuretic peptide. Characterization of the gene and peptide.
 A.Reference number: J54400; MUID:92275775; PMID:1339402
 A.Accession: J54400
 A.Status: translated from GB/EMBL/DBJ
 A.Molecule type: DNA
 A.Residues: 1-126 <RES>
 A.Cross-references: UNIPARC:UPI0000033C91; GB:D90337; NID:G219542; PIDN:BA14351.1; PID
 C.Genetics:
 A.Gene: GDB:NPPC
 A.Cross-references: GDB:250346; OMIM:600296
 A.Map position: 2pter-2qter
 A.Introns: 30/3
 C.Superfamily: natriuretic peptide C precursor
 C.Keywords: brain; diuretic; hormone; natriuretic; neuropeptide; osmoregulation
 F.1-23/Domain: signal sequence #status predicted <SIG>
 F.74-126/Product: natriuretic peptide C-53 #status predicted <CS3>
 F.98-126/Product: natriuretic peptide C-29 #status experimental <C29>
 F.105-126/Product: natriuretic peptide C-22 #status predicted <C22>
 F.110-126/Disulfide bonds: #status predicted

Query Match 80.9%; Score 55; DB 1; Length 126;
 Best Local Similarity 58.8%; Pred. No. 0.00015;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
 DB 110 CFGKLKDRIGSMGSLGC 126

RESULT 20

A55688
 natriuretic peptide C precursor - mouse
 C.Species: Mus musculus (house mouse)
 C.Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004
 C.Accession: A55688
 R.Ogawa, Y.; Itoh, H.; Yoshitake, Y.; Inoue, M.; Yoshimasa, T.; Serikawa, T.; Nakao, K.
 Genomics 24, 383-387, 1994
 A.Title: Molecular cloning and chromosomal assignment of the mouse C-type natriuretic pe
 A.Reference number: A55688; MUID:95213034; PMID:7698765
 A.Accession: A55688
 A.Status: preliminary; not compared with conceptual translation
 A.Molecule type: DNA
 A.Residues: 1-126 <OGA>
 A.Cross-references: UNIPROT:O61839; UNIPARC:UPI0000003FF3; GB:D28873; NID:G633087; PIDN
 C.Genetics:
 A.Gene: NPPC
 C.Superfamily: natriuretic peptide C precursor

Query Match 80.9%; Score 55; DB 2; Length 126;
 Best Local Similarity 58.8%; Pred. No. 0.00015;
 Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFGXXXDRIGXXSXXGC 17
 DB 110 CFGKLKDRIGSMGSLGC 126

RESULT 21

S12988
 brain natriuretic peptide type C - rat
 C.Species: Rattus norvegicus (Norway rat)
 C.Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C.Accession: S12988
 R.Kojima, M.; Minamino, N.; Kangawa, K.; Matsuo, H.
 FEBS Lett. 276, 209-213, 1990
 A.Title: Cloning and sequence analysis of a cDNA encoding a precursor for rat C-type nat
 A.Reference number: S12988; MUID:91092420; PMID:1702395
 A.Accession: S12988
 A.Molecule type: mRNA
 A.Residues: 1-126 <KOJ>
 A.Cross-references: UNIPROT:P55207; UNIPARC:UPI0000125AB2; GB:D90219; NID:G220711; PIDN
 C.Superfamily: natriuretic peptide C precursor

```

Query Match 55.1% Score 55.1 DB 2: Length 126;
Best Local Similarity 58.8%; Pred. NO. 0.00015;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CPGXXXDRIGXXSXGC 17
      ||| ||| ||| |||
DB 110 CFGKLDRIGMSGGLGC 126

RESULT 22
A54119
c-type natriuretic peptide I precursor - bullfrog
N:Alternate names: CNP I
C:Species: Rana catesbeiana (bullfrog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A54119
R:Kojima, M.; Ohnawa, Y.; Miyamoto, K.; Minamino, N.; Kangawa, K.; Matsuo, H.
J. Biol. Chem. 269, 13136-13140, 1994
A>Title: Cloning and characterization of a novel natriuretic peptide in frog (Rana catesbeiana)
A:Reference number: A54119; MUID:94230409; PMID:8175740
A:Accession: A54119
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <KOJ>
A:Cross-references: UNIPROT:P20968; UNIPARC:UPI0000125AE1; GB:D17413; NID:G397837; PIDN:CSuperfamily: natriuretic peptide A precursor

Query Match 80.9%; Score 55; DB 1; Length 129;
Best Local Similarity 58.8%; Pred. NO. 0.00015;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CPGXXXDRIGXXSXGC 17
      ||| ||| ||| |||
DB 113 CFGVCLDRIGAFSGGLGC 129

RESULT 23
A51676
brain natriuretic factor precursor - pig
N:Alternate names: brain natriuretic factor 32
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 09-Jul-2004
C:Accession: A51676; A51517; S06359
R:Maekawa, K.; Sudoh, T.; Futusawa, M.; Minamino, N.; Kangawa, K.; Ohkubo, H.; Nakashima, K.;
Biochem. Biophys. Res. Commun. 157, 410-416, 1988
A>Title: Cloning and sequence analysis of cDNA encoding a precursor for porcine brain natriuretic factor
A:Reference number: A51676; MUID:89061444; PMID:3196348
A:Accession: A51676
A:Molecule type: mRNA
A:Residues: 1-131 <MAE>
A:Cross-references: UNIPROT:P07634; UNIPARC:UPI00001561A8; GB:M23596; NID:G535704; PIDN:R:Sudoh, T.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 155, 726-732, 1988
A>Title: Brain natriuretic peptide-32: N-terminal six amino acid extended form of brain natriuretic factor
A:Reference number: A51517; MUID:88339957; PMID:3421965
A:Accession: A51517
A:Molecule type: protein
A:Residues: 100-131 <SUD>
A:Cross-references: UNIPARC:UPI000003520D
R:Sudoh, T.; Kangawa, K.; Minamino, N.; Matsuo, H.
Nature 332, 78-81, 1988
A>Title: A new natriuretic peptide in porcine brain.
A:Reference number: S06359; MUID:88156915; PMID:2964562
A:Accession: S06359
A:Molecule type: protein
A:Residues: 106-131 <SUD>
A:Cross-references: UNIPARC:UPI000003520C
C:Superfamily: natriuretic peptide A precursor
C:Keywords: brain; natriuretic
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-131/Product: brain gamma natriuretic factor #status predicted <GAM>
F:100-131/Product: brain alpha natriuretic peptide #status experimental <ALF>
F:109-125/Dissulfide Bonds: #status experimental

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Query Match 55: DB 2; Length 131;
Best Local Similarity 58.8%; Pred. No. 0.00016;
Matches 10; Conservative 0; Mismatches 7; Indels 0;
Gaps 0;

1 CFCGXXDRIGKXXSXXGC 17
||| ||||| ||
Db 109 CFCGRLDRIGSLSLGCG 125

RESULT 24
A33873
brain natriuretic peptide precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 09-Jul-2004
C:Accession: A33873; A31675
R:Porter, J.G.; Artstein, A.; Palisi, T.; Scarborough, R.M.; Lewicki, J.A.; Seilhamer, J.
R: Biol. Chem. 264, 6689-6692, 1989
A:Title: Cloning of a cDNA encoding porcine brain natriuretic peptide.
A:Reference number: A33873; MUID:89214071; PMID:2708334
A:Accession: A33873
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-131 <PDB>
A:Cross-references: UNIPROT:P07634; UNIPARC:UPI0000125ADB; GB:M25547; GB:J04708; GB:M222
B:Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 157, 402-409, 1988
A:Title: Isolation and identification of a high molecular weight brain natriuretic peptide.
A:Reference number: A31675; MUID:89061743; PMID:3196347
A:Accession: A31675
A:Status: preliminary
A:Molecule type: protein
A:Residues: 26-131 <MIN>
A:Cross-references: UNIPARC:UPI000017657F
C:Superfamily: natriuretic peptide A precursor

Query Match 58.8%; Score 55; DB 2; Length 131;
Best Local Similarity 58.8%; Pred. No. 0.00016;
Matches 10; Conservative 0; Mismatches 7; Indels 0;
Gaps 0;

1 CFCGXXDRIGKXXSXXGC 17
||| ||||| ||
Db 109 CFCGRLDRIGSLSLGCG 125

RESULT 25
A61244
natriuretic peptide type C precursor - spiny dogfish
C:Species: Squalus acanthias (spiny dogfish)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A61244; I51329
R:Schofield, J.P.; Jones, D.S.C.; Forrest Jr., J.N.
Am. J. Physiol. 261, F734-F739, 1991
A:Title: Identification of C-type natriuretic peptide in heart of spiny dogfish shark (
A:Reference number: A61244; MUID:92026459; PMID:1928383
A:Accession: A61244
A:Molecule type: mRNA
A:Residues: 1-135 <SCH>
A:Cross-references: UNIPROT:P41319; UNIPARC:UPI0000125AE5; EMBL:X59991, NID:g556803, PI
C:Genetics:
A:introns: 30/3
C:Superfamily: natriuretic peptide A precursor
C:Keywords: diuretic bond; diuretic; hormone; natriuretic; osmoregulation
F:1-25/Domain: signal sequence #status predicted <SIG>
F:114-135/Product: natriuretic peptide C #status predicted <NPC>
F:119-135/Disulfide bonds: #status predicted

Query Match 80.9%; Score 55; DB 1; Length 135;
Best Local Similarity 58.8%; Pred. No. 0.00016;
Matches 10; Conservative 0; Mismatches 7; Indels 0;
Gaps 0;

1 CFCGXXDRIGKXXSXXGC 17
||| ||||| ||

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Db 119 CFCGLKLDRIQAMSGLGC 135

RESULT 26

S14320
alpha-atrial natriuretic peptide precursor - chicken

C:Species: Gallus gallus (chicken)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: S14320; A:1509

R:Akiyuki, N.; Kangawa, K.; Minamino, N.; Matsuo, H.

FEBS Lett. 280, 357-362, 1991

A:Title: Cloning and sequence analysis of complementary DNA encoding a precursor for chicken atrial natriuretic peptide

A:Reference number: S14320; MUID:91192169; PMID:1826483

A:Accession: S14320

A:Reference number: S14320

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-140 <AKI>

A:Cross-references: UNIPROT:P18908; UNIPARC:UPI0000125AFA; GB:X57702; NID:g53648; PIDN:C

R:Miyaoka, A.; Minamino, N.; Kangawa, K.; Matsuo, H.

Biochem. Biophys. Res. Commun. 155, 1330-1337, 1988

A:Title: Identification of a 29-amino acid natriuretic peptide in chicken heart.

A:Reference number: A31509; MUID:89025805; PMID:2972278

A:Accession: A31509

A:Molecule type: protein

A:Residues: 112-140 <MTY>

A:Cross-references: UNIPARC:UPI00000351BC

C:Superfamily: natriuretic peptide A precursor

F:118-134/Disulfide bonds: #status experimental

Query Match 80.9%; Score 55; DB 1; Length 140;
Best Local Similarity 58.8%; Pred. No. 0.00016;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFCGXXDRIGXXSXGC 17
118 CFCGRRIDRIGSLGMC 134

RESULT 27

AMDG

atrial natriuretic peptide precursor - dog

N:Alternate names: ANP; atrial natriuretic polypeptide

C:Species: Canis lupus familiaris (dog)

C>Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004

C:Accession: A25302

R:Oikawa, S.; Imai, M.; Inuzuka, C.; Tawaragi, Y.; Nakazato, H.; Matsuo, H.

Biochem. Biophys. Res. Commun. 132, 892-899, 1985

A:Title: Structure of dog and rabbit precursors of atrial natriuretic polypeptides deduced from complementary DNA

A:Reference number: A90119; MUID:86076957; PMID:2934062

A:Accession: A25302

A:Molecule type: mRNA

A:Residues: 1-149 <OIK>

A:Cross-references: UNIPROT:P07499; UNIPARC:UPI0000125AF8; GB:M12045; NID:g163900; PIDN:

C:Superfamily: natriuretic peptide A precursor

C:Keyword: atrium; diuretic; hormone; natriuretic; osmoregulation

F:1-23/Domain: signal sequence #status predicted <SIG>

F:124-149/Product: gamma atrial natriuretic factor #status predicted <ANP>

F:128-149/Product: alpha atrial natriuretic peptide #status predicted <ANP>

F:128-144/Disulfide bonds: #status predicted

Query Match 80.9%; Score 55; DB 1; Length 149;
Best Local Similarity 58.8%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFCGXXDRIGXXSXGC 17
128 CFCGRMDRIGAGSLGC 144

RESULT 28

S13107
atrial natriuretic peptide precursor - pig

N:Contains: alpha atrial natriuretic peptide; gamma atrial natriuretic factor (cardiotoni

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 21-Nov-1993 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004

C:Accession: S13107; A:60899

R:Maegest, H.J.; Appelhaus, H.; Gaseen, H.G.; Forssmann, W.G.

Nucleic Acids Res. 18, 6704, 1990

A:Title: Nucleotide sequence of a porcine prepro atrial natriuretic peptide (ANP) cDNA.

A:Reference number: S13107; MUID:91067478; PMID:2147477

A:Accession: S13107

A:Molecule type: mRNA

A:Residues: 1-150 <MAE>

A:Cross-references: UNIPROT:P24259; UNIPARC:UPI0000125AFD; EMBL:X54669; NID:g1863; PIDN

R:Forssmann, W.G.; Hock, D.; Lotzspiech, A.; Henschen, A.; Kreye, V.; Christmann, M.; Re

Anat. Embryol. 168, 307-313, 1983

A:Title: The right auricle of the heart is an endocrine organ. Cardiotonic as a peptide

A:Reference number: A60899; MUID:84176555; PMID:6689515

A:Accession: A60899

A:Molecule type: protein

A:Residues: 25-54 <FOR>

A:Cross-references: UNIPARC:UPI00001733A9

C:Superfamily: natriuretic peptide A precursor

C:Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-150/Product: gamma atrial natriuretic factor #status predicted <ANP>

F:123-150/Product: alpha atrial natriuretic peptide #status predicted <ANP>

F:129-145/Disulfide bonds: #status predicted

Query Match 80.9%; Score 55; DB 1; Length 150;
Best Local Similarity 58.8%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CFCGXXDRIGXXSXGC 17
129 CFCGRMDRIGAGSLGC 145

RESULT 29

AMHU

natriuretic peptide A precursor (validated) - human

N:Alternate names: ANP; atrial natriuretic factor; atrial natriuretic protein; prepronat

N:Contains: atrial alpha natriuretic peptide (ANP); cardiotonic (atrial gamma natriure

C:Species: Homo sapiens (man)

C>Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004

C:Accession: A22693; B22693; A01424; B29370; A32733; I58054; S14097; I39458; I39

R:Nemer, M.; Chamberland, M.; Strols, D.; Argentin, S.; Drouin, J.; Dixon, R.A.F.; Zivin

Nature 312, 654-656, 1984

A:Title: Gene structure of human cardiac hormone precursor, pronatriuretic

A:Reference number: A22693; MUID:85061626; PMID:6095118

A:Accession: A22693

A:Molecule type: DNA

A:Residues: 1-151 <NEM>

A:Cross-references: UNIPROT:P01160; UNIPARC:UPI0000000DC4; GB:X01470; NID:g28687; PIDN:

A:Accession: B22693

A:Molecule type: DNA

A:Residues: 1-151, 'RR', <NE2>

A:Cross-references: UNIPARC:UPI0000125AF6

A:Note: allelic variant with UGA termination codon replaced by CGA arginine codon

R:Oikawa, S.; Imai, M.; Ueno, A.; Tanaka, S.; Noguchi, T.; Nakazato, H.; Kangawa, K.; Fu

Nature 309, 724-726, 1984

A:Title: Cloning and sequence analysis of cDNA encoding a precursor for human atrial nat

A:Reference number: A01424; MUID:84219799; PMID:6203042

A:Accession: A01424

A:Molecule type: mRNA

A:Residues: 1-151 <OIK>

A:Cross-references: UNIPARC:UPI0000000DC4; GB:X02043; NID:g178629; PIDN:AA859379.1; PID

R:Seidman, C.E.; Bloch, K.D.; Klein, K.A.; Smith, J.A.; Seidman, J.G.

Science 226, 1206-1209, 1984

A:Title: Nucleotide sequences of the human and mouse atrial natriuretic factor genes.

A:Reference number: A29370; MUID:85065766; PMID:6542248

A:Accession: B29370

A:Molecule type: DNA

A:Residues: 1-64, 'D', '66-151 <SEI>

A:Cross-references: UNIPARC:UPI000016A557; GB:X02043

R:Kangawa, K.; Matsuo, H.

Biochem. Biophys. Res. Commun. 118, 131-139, 1984
A>Title: Purification and complete amino acid sequence of alpha-human atrial natriuretic peptide
A:Reference number: A32733; MUID:84128019; PMID:6230082
A:Accession: A32733
A:Molecule type: protein
A:Residues: 124-151 <KAN>
A:Cross-references: UNIPARC:UPI000002B7D3
R.Nakayama, K.; Ohkubo, H.; Hirose, T.; Inayama, S.; Nakanishi, S.
Nature 310, 699-701, 1984
A>Title: mRNA sequence for human cardiolipin-atrial natriuretic factor precursor and 1
A:Reference number: 158054; MUID:84295577; PMID:6547996
A:Accession: 158054
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-151 <RES>
A:Cross-references: UNIPARC:UPI000000DCD4; GB:M30262; NID:g180181; PIDN:AAA5669.1; PID
R.Vansteede, Y.; Michel, A.; Deschodt-Lanckman, M.
Eur. J. Biochem. 196, 281-286, 1991
A>Title: Hydrolysis of intact and Cys-Phe-cleaved human atrial natriuretic peptide in v
A:Reference number: S14097; MUID:91176998; PMID:1826098
A:Accession: S14097
A:Molecule type: protein
A:Residues: 124-151 <VAN>
A:Cross-references: UNIPARC:UPI000002B7D3
A>Note: natural and synthetic peptide subjected to kallikrein proteolysis
R.Zivian, R.A.; Condra, J.H.; Dixon, R.A.; Seidman, N.G.; Chretien, M.; Nemer, M.; Chambe
Proc. Natl. Acad. Sci. U.S.A. 81, 6325-6329, 1984
A>Title: Molecular cloning and characterization of DNA sequences encoding rat and human
A:Reference number: 139458; MUID:85038509; PMID:6238331
A:Accession: 139458
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 119-151, 'RR', <RE2>
A:Cross-references: UNIPARC:UPI000002DD32; GB:K02044; NID:g178631; PIDN:AAA51730.1; PID
R.Maki, M.; Parentier, M.; Inagami, T.
Biochem. Biophys. Res. Commun. 125, 797-802, 1984
A>Title: Cloning of genomic DNA for human atrial natriuretic factor.
A:Reference number: 139459; MUID:85096983; PMID:6097248
A:Accession: 139459
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-75 <RE3>
A:Cross-references: UNIPARC:UPI000016A556; GB:K02399; NID:g178633; PIDN:AAA35528.1; PID
R.Seidman, C.E.; Bloch, R.D.; Zisfein, J.; Smt, J.; Haber, E.; Homcy, C.J.; Duby, A.D.
Hypertension 7, 31-34, 1985
A>Title: Molecular studies of the atrial natriuretic factor gene.
A:Reference number: 139460
A:Accession: 139460
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-64, 'D', '66-151 <RE4>
A:Cross-references: UNIPARC:UPI000016A557; GB:M54951; NID:g178636; PIDN:AAA35529.1; PID
R.Greene, B.D.; Benzon, G.H.; Seilhammer, U.J.; Lewicki, J.A.; Fiddes, J.C.
Nature 312, 655-658, 1984
A>Title: Nucleotide sequence of the gene encoding human atrial natriuretic factor precursor
A:Reference number: 137167; MUID:85061627; PMID:6095119
A:Accession: 137167
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 26-151 <RE5>
A:Cross-references: UNIPARC:UPI0000156DAE; EMBL:X01471; NID:g28690; PIDN:CAA25700.1; PID
C:Comment: Cardiolipin is a vasoconstrictor but not a diuretic or natriuretic.
C:Genetics:
A:Gene: GDB:ANPA; ANP; PND
A:Cross-references: GDB:118727; OMIM:108780
A:Map position: 1P36-1P36
A:Introns: 41/3; 150/3
C:Superfamily: natriuretic peptide A precursor
C:Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation
F:1-25/Domain: signal sequence #status predicted <IG>
F:26-151/Product: cardiolipin #status predicted <CD>
F:124-151/Product: atrial alpha natriuretic peptide #status experimental <ANP>
F:120-146/Dissulfide bonds: #status experimental

```

Query Match 100.0% Score 55; DB 1; Length 151;
Best Local Similarity 58.8%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

1 CFGXXXXRIGXXSXXGC 17
DB 130 CFGGRMDRIGAGSLGC 146

RESULT 30
AMMO
atrial natriuretic peptide precursor - bovine
N.Alternate names: ANP; atrial natriuretic polypeptide
C.Species: Bos primigenius taurus (cattle)
C.Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C.Accession: A90124; A93049; A24247; A26090
R.Vlasuk, G.P.; Miller, J.; Bencan, G.H.; Lewicki, J.A.
Biochem. Biophys. Res. Commun. 136, 396-403, 1986
A.Title: Structure and analysis of the bovine atrial natriuretic peptide precursor gene
A.Reference number: A90124; MUID:86215205; PMID:2939830
A.Accession: A90124
A.Molecule type: DNA
A.Residues: 1-152 <VLA>
A.Cross-references: UNIPROT:P07501; UNIPARC:UPI0000125AF7; GB:M13145; NID:G162665; PID:R10ng; H.; McNICOLL, N.; Lazure, C.; Seidman, N.; Chretien, M.; Cantin, M.; De Lean, A. Life Sci. 38, 1309-1315, 1986
A.Title: Purification and sequence determination of bovine atrial natriuretic factor.
A.Reference number: A93049; MUID:86173941; PMID:3007908
A.Accession: A93049
A.Molecule type: protein
A.Residues: 123-150 <ONG>
A.Cross-references: UNIPARC:UPI00002B7D3
C.Genetics:
A.Introns: 40/3; 149/3
C.Superfamily: natriuretic peptide A precursor
C.Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation
F.1-24/Domain: signal sequence #status predicted <SIG>
F.123-152/Product: gamma atrial natriuretic factor #status predicted <ANF>
F.123-150/Product: alpha atrial natriuretic peptide #status experimental <ANP>
F.129-145/Dissulfide bonds: #status predicted

Query Match 80.9%; Score 55; DB 1; Length 152;
Best Local Similarity 58.8%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

1 CFGXXXXRIGXXSXXGC 17
DB 129 CFGGRMDRIGAGSLGC 145

RESULT 31
AMMS
atrial natriuretic peptide precursor - mouse
C.Species: Mus musculus (house mouse)
C.Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C.Accession: A29370; B43619
R.Seidman, C.E.; Bloch, K.D.; Klein, K.A.; Smith, J.A.; Seidman, J.G.
Science 226, 1206-1209, 1984
A.Title: Nucleotide sequences of the human and mouse atrial natriuretic factor genes.
A.Reference number: A29370; MUID:85065766; PMID:6542248
A.Accession: A29370
A.Molecule type: DNA
A.Residues: 1-152 <STI>
A.Cross-references: UNIPROT:P05125; UNIPARC:UPI0000027BFB; GB:K02781; NID:G191937; PID:
C.Genetics:
A.Introns: 40/3; 149/3
C.Superfamily: natriuretic peptide A precursor
C.Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation
F.1-24/Domain: signal sequence #status predicted <SIG>
F.25-150/Product: gamma atrial natriuretic factor #status predicted <ANF>
F.123-150/Product: alpha atrial natriuretic peptide #status predicted <ANP>
F.129-145/Dissulfide bonds: #status predicted

```

Query Match 80.9%; Score 55; DB 1; Length 152;
Best Local Similarity 58.8%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 CFCGXXDRIGGXXSGC 17
Db 129 CFCGRIDRIGAGSGG 145
RESULT 32
AMRT
atrial natriuretic factor precursor - rat
N:Contains: ANF(1-33); ANF(2-33); ANF(3-33); ANF(8-33); atrial natriuretic peptide; atr
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-Feb-1984 #sequence revision 15-Nov-1984 #text change 09-Jul-2004
C:Accession: A22570; A01425; A93332; A43617; A93330; A94275; P70061; A20973; A44190; A60
R:Argentin, S.; Nemer, M.; Drouin, J.; Scott, G.K.; Kennedy, B.P.; Davies, P.L.
J. Biol. Chem. 260, 4568-4571, 1985
A:Title: The gene for rat atrial natriuretic factor.
A:Reference number: A22570; MUID:85182558; PMID:2985557
A:Accession: A22570
A:Molecule type: DNA
A:Residues: 1-152 <ARG>
A:Cross-references: UNIPROT:P01151; UNIPARC:UPI0000125B00; GB:K02062; NID:9202899; PIDN:
R.Yamanaka, M.; Greenberg, B.; Johnson, L.; Sellhammer, J.; Brewer, M.; Friedemann, T.; W
Nature 309, 719-722, 1984
A:Title: Cloning and sequence analysis of the cDNA for the rat atrial natriuretic factor
A:Reference number: A93331, MUID:84219797; PMID:6547210
A:Accession: A01425
A:Molecule type: mRNA
A:Residues: 1-152 <YAM>
A:Cross-references: UNIPARC:UPI0000125B00; EMBL:X00665; NID:955711; PIDN:CAA2585.1; PID
R.Maki, M.; Takayanagi, R.; Misono, K.S.; Pandey, K.N.; Tibbitts, C.; Inagami, T.
Nature 309, 722-724, 1984
A:Title: Structure of rat atrial natriuretic factor precursor deduced from cDNA sequence
A:Reference number: A93332; MUID:84219798; PMID:6328328
A:Accession: A93332
A:Molecule type: mRNA
A:Residues: 1-152 <MAK>
A:Cross-references: UNIPARC:UPI0000125B00; GB:X00665; EMBL:X00658; NID:955711; PIDN:CAA2
R.Seidman, C.E.; Duby, A.D.; Choi, E.; Graham, R.M.; Haber, E.; Homcy, C.; Smith, J.A.;
Science 225, 324-326, 1984
A:Title: The structure of rat preproatrial natriuretic factor as defined by a complement
A:Reference number: A43617; MUID:84250178; PMID:6234658
A:Accession: A43617
A:Molecule type: mRNA
A:Residues: 1-152 <SEI>
A:Cross-references: UNIPARC:UPI0000125B00; GB:K02062; GB:K02063; NID:9202899; PIDN:AAA40
R.Acllas, S.A.; Kleihert, H.D.; Camargo, M.J.; Januszewicz, A.; Sealey, J.E.; Latagh, J.H
Nature 309, 717-719, 1984
A:Title: Purification, sequencing and synthesis of natriuretic and vasoactive rat atrial
A:Reference number: A93330, MUID:84219796; PMID:6233494
A:Accession: A93330
A:Molecule type: protein
A:Residues: 126-149 <ATL>
A:Cross-references: UNIPARC:UPI00000351FC
R.Currie, M.G.; Geller, D.M.; Cole, B.R.; Siegel, N.R.; Fok, K.F.; Adams, S.P.; Eubanks,
Science 223, 67-69, 1984
A:Title: Purification and sequence analysis of bioactive atrial peptides (atriopeptins).
A:Reference number: A94275; MUID:84097513; PMID:6419347
A:Accession: A94275
A:Molecule type: protein
A:Residues: 127-149 <CUR>
A:Cross-references: UNIPARC:UPI00000351PB
R.Thibault, G.; Murphy, K.K.; Gutkowska, J.; Seidah, N.G.; Lazure, C.; Chretien, M.; Car
Peptides 9, 47-53, 1988
A:Title: NH2-terminal fragment of rat pro-atrial natriuretic factor in the circulation.
A:Reference number: P70061, MUID:88203350; PMID:2966345
A:Accession: P70061
A:Molecule type: protein
A:Residues: 25-28, 'X', 30-31, 'X', 33, 'X', 35-38 <THI>
A:Cross-references: UNIPARC:UPI00001733AA

R.Seidah, N.G.; Lazure, C.; Chretien, M.; Thibault, G.; Garcia, R.; Cantin, M.; Genest,
Proc. Natl. Acad. Sci. U.S.A. 81, 2640-2644, 1984
A:Title: Amino acid sequence of homologous rat atrial peptides: natriuretic activity of
A:Reference number: A20973; MUID:84194062; PMID:6232612
A:Accession: A20973
A:Molecule type: protein
A:Residues: 118-150 <SE2>
A:Cross-references: UNIPARC:UPI000002BE79
R.Flynn, T.G.; Davies, P.L.; Kennedy, B.P.; de Bold, M.L.; de Bold, A.J.
Science 228, 323-325, 1985
A:Title: Alignment of rat cardionatrin sequences with the preprocardionatrin sequence fr
A:Reference number: A44190; MUID:85168263; PMID:3157217
A:Accession: A44190
A:Molecule type: mRNA
A:Residues: 1-152 <FLY>
A:Cross-references: UNIPARC:UPI0000125B00; GB:K02062; NID:9202899; PIDN:AAA40735.1; PID
A:Note: part of this sequence, including the amino ends of three mature peptides, was co
R.Belcourt, D.; Varmuza, D.R.; Toney, K.; Bennett, H.P.J.
Protein Expr. Purif. 1, 28-32, 1990
A:Title: Purification of rat pro-atrial natriuretic factor: a simplified scheme using re
A:Reference number: A60390; MUID:93044510; PMID:2152180
A:Accession: A60390
A:Molecule type: protein
A:Residues: 25-39 <BEL>
A:Cross-references: UNIPARC:UPI0000066C9
R.Gardner, D.G.; Vlasuk, G.P.; Baxter, J.D.; Fiddes, J.C.; Lewicki, J.A.
Proc. Natl. Acad. Sci. U.S.A. 84, 2175-2179, 1987
A:Title: Identification of atrial natriuretic factor gene transcripts in the central ner
A:Reference number: I59094; MUID:87175636; PMID:2951736
A:Accession: I59094
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 38-152 <RES>
A:Cross-references: UNIPARC:UPI0000170882; GB:M15868; NID:9202903; PIDN:AAA40736.1; PID
R.Kangawa, K.; Tawarayagi, Y.; Oikawa, S.; Mizuno, A.; Sakuragawa, Y.; Nakazato, H.; Fukud
Nature 312, 152-155, 1984
A:Title: Identification of rat gamma atrial natriuretic polypeptide and characterization
A:Reference number: I58057; MUID:85061500; PMID:6239103
A:Accession: I58057
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-152 <RE2>
A:Cross-references: UNIPARC:UPI0000125B00; EMBL:X01118; NID:955716; PIDN:CAA25586.1; PID
R.Flynn, T.G.
Can. J. Physiol. Pharmacol. 65, 2013-2020, 1987
A:Title: The elucidation of the structure of atrial natriuretic factor, a new peptide hc
A:Reference number: I52678; MUID:88109092; PMID:2962707
A:Accession: I52678
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-51, 'X', 53-85, 'X', 87-152 <RE3>
A:Cross-references: UNIPARC:UPI0000170883; GB:M27498; NID:9202905; PIDN:AAA40737.1; PID
C:Comment: A disulfide bond is required for full activity of atriopeptin.
C:Comment: Several active peptides may be derived from the carboxyl region of this prec
C:Genetics:
A:Gene: ANF
A:Introns: 40/3; 149/3
C:Superfamily: natriuretic peptide A precursor
C:Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation
F:1-24/Domain: signal sequence #status predicted <Sig>
F:25-152/Product: pro-atrial natriuretic factor #status experimental <Pro>
F:25-150/Product: cardionatrin IV #status experimental <CN4>
F:73-150/Product: cardionatrin III #status experimental <CN3>
F:118-150/Product: ANF(1-33) #status experimental <ANF1>
F:119-150/Product: ANF(2-33) #status experimental <ANF2>
F:120-150/Product: ANF(3-33) #status experimental <ANF3>
F:123-150/Product: cardionatrin I #status experimental <CN1>
F:125-150/Product: ANF(8-33) #status experimental <ANF4>
F:126-150/Product: auriculatin B #status experimental <AUB>
F:127-150/Product: auriculatin A #status experimental <AUA>
F:127-150/Product: atrial natriuretic factor #status predicted <MAT>
F:127-149/Product: atriopeptin I #status experimental <AT1>
F:127-147/Product: atriopeptin II #status experimental <AT2>

C;Date: 02-Jul-1996 #sequence_revision 05-Sep-1996 #text_change 20-Oct-2000

Keywords: brain; diuretic; hormone; natriuretic; osmoregulation

F,1-26/Domain: signal sequence #stratus predicted <StG>
C;keywords: brain; diuretic; hormone; hatriuretic; osmoregulation

C;Accession: T34850
R/Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

F:27-426/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

F.534-815/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
 F.1443-1732/Domain: long-chain alcohol dehydrogenase homology <LADH>
 F.1764-1944/Domain: short-chain alcohol dehydrogenase homology <SADH>
 F.2015-2095/Domain: acyl carrier protein homology <ACP1>

Query Match 51.5%; Score 35; DB 2; Length 2110;
 Best Local Similarity 54.5%; Pred. No. 41;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 7 DRIGXXSXGC 17
 DB 1501 DRVGFSSEGC 1511

RESULT 42

A70668
 mycocerosate synthase (EC 2.3.1.111) - Mycobacterium tuberculosis

C/Species: Mycobacterium tuberculosis
 C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C/Accession: A70668

R/Colo: S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998

A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A/Reference number: A70500; PMID:98295987; PMID:9634230

A/Accession: A70668
 A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-2111 <COL>

A/Cross-references: UNIPROT:P96291; UNIPARC:UPI0000036BA0; GB:Z83658; GB:AL123456; NID:G

A/Experimental source: strain H37RV

C/Genetics:

A/Gene: mas

C/Suprafamily: mycocerosic acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I h
 nase homology; [acyl-carrier-protein] S-malonyltransferase homology

C/Keywords: acyltransferase; carrier protein; coenzyme A; phosphotransferase

F.27-426/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

F.534-815/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>

F.1444-1733/Domain: long-chain alcohol dehydrogenase homology <LADH>

F.1765-1945/Domain: short-chain alcohol dehydrogenase homology <SADH>

F.2016-2096/Domain: acyl carrier protein homology <ACP1>

Query Match 51.5%; Score 35; DB 2; Length 2111;
 Best Local Similarity 54.5%; Pred. No. 41;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 7 DRIGXXSXGC 17
 DB 1502 DRVGFSSEGC 1512

RESULT 43
 C86926
 probable mycocerosic synthase [imported] - Mycobacterium leprae

C/Species: Mycobacterium leprae
 C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C/Accession: C86926

R/Colo: S.T.; Eiglsmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
 R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltham, T.; Fraser, A.; Hamlin, N.; Holtroyd,
 eam, M.A.; Rutherford, K.M.
 Nature 409, 1007-1011, 2001

A/Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq

A/Title: Massive gene decay in the leprosy bacillus.

A/Reference number: A86909; PMID:21128732; PMID:11234002

A/Accession: C86926

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-2116 <STO>

A/Cross-references: UNIPROT:Q9CD78; UNIPARC:UPI00000C6C57; GB:AL450380; NID:G13092517; F

C/Genetics:

A/Gene: mas

C/Suprafamily: mycocerosic acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I
 nase homology; [acyl-carrier-protein] S-malonyltransferase homology

C/Keywords: carrier protein

Query Match 51.5%; Score 35; DB 2; Length 2116;
 Best Local Similarity 54.5%; Pred. No. 41;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 7 DRIGXXSXGC 17
 DB 1500 DRVGFSSEGC 1510

RESULT 44

S72705
 mycocerosate synthase (EC 2.3.1.111) - Mycobacterium leprae

N/Alternate names: Lep1170_C2_209 protein

C/Species: Mycobacterium leprae

C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C/Accession: S72705

R/Smith, D.R.; Robison, K.

submitted to the EMBL Data Library, November 1993

A/Description: Mycobacterium leprae cosmid B1170.

A/Reference number: S72693

A/Accession: S72705

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-2118 <SMT>

A/Cross-references: UNIPROT:Q49624; UNIPARC:UPI00000CA943; EMBL:U00010; NID:G466780; P

C/Genetics:

A/Start codon: TTG

C/Suprafamily: mycocerosic acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I
 nase homology; [acyl-carrier-protein] S-malonyltransferase homology

C/Keywords: acyltransferase; carrier protein; coenzyme A

F.28-426/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

F.536-816/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>

F.1449-1738/Domain: long-chain alcohol dehydrogenase homology <LADH>

F.1770-1954/Domain: short-chain alcohol dehydrogenase homology <SADH>

F.2038-2110/Domain: acyl carrier protein homology <ACP1>

Query Match 51.5%; Score 35; DB 2; Length 2118;
 Best Local Similarity 54.5%; Pred. No. 41;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 7 DRIGXXSXGC 17
 DB 1507 DRVGVSBNQC 1517

RESULT 45
 A11422
 hypothetical protein bvrC [imported] - Listeria monocytogenes (strain EGD-e)

C/Species: Listeria monocytogenes

C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C/Accession: A11422

R/Glaeser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeck

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Fsihi, I

S.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A/Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; f

ok, C.; Schueller, T.; Simoes, N.; Tietzer, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlan

A/Title: Comparative genomics of Listeria species.

A/Reference number: A11077; PMID:21537279; PMID:11679669

A/Accession: A11422

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-327 <GLA>

A/Cross-references: UNIPROT:Q8V3P8; UNIPARC:UPI00000556DD; GB:NC_003210; PIDN:CAD00999

A/Experimental source: strain EGD-e

C/Genetics:

A/Gene: bvrC

C/Suprafamily: ADP-ribosylglycohydrolase

Query Match 50.0%; Score 34; DB 2; Length 327;
 Best Local Similarity 41.2%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

1 CFCGXXDRIGXXSXXGC 17
 ||| | | | | | | | | | | | | | | | | | | | |
 Db 276 CIGMDPTDTCGALSAGIC 292

RESULT 46

H97462

hypothetical protein AGR_C1553 [imported] - Agrobacterium tumefaciens (strain C58, Cere

C/Species: Agrobacterium tumefaciens

C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #ext_change 09-Jul-2004

C/Accession: H97462

R/Goodner, B.; Hinkle, G.; Galtung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A/Reference number: A97359; MUID:21608551; PMID:11743194

A/Accession: H97462

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-504 <KUR>

A/Cross-references: UNIPROT:Q8UH35; UNIPARC:UPI00000D1953; GB:AE007869; PIDN:AAK86657.1;

C/Genetics:

A/Gene: AGR_C1553

A/Map position: circular chromosome

Query Match 50.0%; Score 34; DB 2; Length 504;
 Best Local Similarity 54.5%; Pred. No. 18;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

7 DRIGXXSXXGC 17
 ||| | | | | | | | | | | | | | | | | | | | |
 Db 29 DRIGVAMAGC 39

RESULT 47

S50856

whn protein - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 14-Jul-1995 #sequence_revision 03-Nov-1995 #ext_change 05-Oct-2004

C/Accession: S50856

R/Neils, M.; Pfeiffer, D.; Schorpp, M.; Hedrich, H.; Boehm, T.

Nature 372, 103-107, 1994

A/Title: New member of the winged-helix protein family disrupted in mouse and rat nude m

A/Reference number: S50856; MUID:95059376; PMID:796402

A/Accession: S50856

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-648 <NEH>

A/Cross-references: UNIPARC:UPI0000020C07; GB:X81593; NID:9563511; PIDN:CAA57279.1; PID:

F:271-364/Domain: fork head DNA-binding domain homology <FHD>

Query Match 50.0%; Score 34; DB 2; Length 648;
 Best Local Similarity 35.3%; Pred. No. 23;
 Matches 6; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

1 CFCGXXDRIGXXSXXGC 17
 ||| | | | | | | | | | | | | | | | | | | | |
 Db 328 CFEKVENKSGSSSRKGC 344

RESULT 48

H70819

probable polyketide synthase - Mycobacterium tuberculosis (strain H37RV)

C/Species: Mycobacterium tuberculosis

C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #ext_change 09-Jul-2004

C/Accession: H70819

R/Coile, S.T.; Broesch, R.; Parhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Comor, R.; Davies, R.; Devlin, K.; Feltsell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A/Reference number: A70500; MUID:98295987; PMID:9634230

A/Accession: H70819

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-2108 <COL>

A/Cross-references: UNIPROT:O53901; UNIPARC:UPI00000D3B08; GB:AL022000; GB:AL123456; NID

A/Experimental source: strain H37RV

C/Genetics:

A/Gene: pks5

C/Supplemental: mycocerosic acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I ho

nase homology; [acyl-carrier-protein] S-malonyltransferase homology

C/Keywords: carrier protein

F:356-434/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <ONS>

F:546-826/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>

F:1444-1733/Domain: long-chain alcohol dehydrogenase homology <LADH>

F:1765-1945/Domain: short-chain alcohol dehydrogenase homology <SADH>

F:2029-2094/Domain: acyl carrier protein homology <ACP1>

Query Match 50.0%; Score 34; DB 2; Length 2108;
 Best Local Similarity 54.5%; Pred. No. 67;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

7 DRIGXXSXXGC 17
 ||| | | | | | | | | | | | | | | | | | | | |
 Db 1502 DRVGMSXNGC 1512

RESULT 49

A97088

uncharacterized protein, homolog of PHN E.coli [imported] - Clostridium acetobutylicum

C/Species: Clostridium acetobutylicum

C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #ext_change 09-Jul-2004

C/Accession: A97088

R/Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo

A/Reference number: A96900; MUID:21359325; PMID:21359325

A/Accession: A97088

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-137 <KUR>

A/Cross-references: UNIPROT:Q971W5; UNIPARC:UPI00000CA223; GB:AE001437; PIDN:AAK79492.1;

A/Experimental source: Clostridium acetobutylicum ATCC824

C/Genetics:

A/Gene: CAC1525

Query Match 48.5%; Score 33; DB 2; Length 137;
 Best Local Similarity 29.4%; Pred. No. 9.4;
 Matches 5; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

1 CFCGXXDRIGXXSXXGC 17
 ||| | | | | | | | | | | | | | | | | | | | |
 Db 119 CIGSLTDKRGIEHFRNC 135

RESULT 50

T10652

hypothetical protein T5F17.30 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #ext_change 09-Jul-2004

C/Accession: T10652

R/Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancro

submitted to the Protein Sequence Database, June 1999

A/Reference number: Z16533

A/Accession: T10652

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-419 <BEV>

A/Cross-references: UNIPROT:Q9M0H3; UNIPARC:UPI00000A7272; EMBL:AL049917; GSPDB:GN00062.

A/Experimental source: cultivar Columbia; BAC clone T5F17

C:Genetics:
 A:Gene: ATSP:TSF17.30
 A:Map position: 4
 A:Introns: 97/1; 243/3; 328/3
 C:Superfamily: Arabidopsis thaliana hypothetical protein F17J16.20

Query Match 48.5%; Score 33; DB 2; Length 419;
 Best Local Similarity 35.3%; Pred. No. 26;
 Matches 6; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 CFCXXXDRIGXSXGC 17
 | | | | |
 Db 53 CLWTRFDRGTGFMEVAGC 69

Search completed: January 26, 2006, 14:45:29
 Job time : 23 secs

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